

FIGURE 1

AGGCGGGCAGCAGCTGCAGGCTGACCTTG CAGCTTGGCGGAATGGACTGGCCTCACAACCTGCTGTTTCTT
CTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAAGAGGAAGGGGCAAGGGCG
GCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACCTGGTGTCACGGATGAAACCGTATGCC
GCATGGAGGAGTATGAGAGGAACATCGAGGAGATGGTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAG
AGAAAGTGTGAGGTCAACTTGCAGCTGTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCAT
CAACCACGACCCAGCCGTATCCCCGTGGACCTGCCGGAGGCACGGTGCCCTGTGTCTGGGCTGTGTGAACC
CCTTACCATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTT CAGCCAGGTTCTGTGCGCCGCCGC
CTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCGCTGTGGGCTG
CACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGACCATCCTCCTTGCACCTTT
GTGCCAAGAAAGGCCCTATGAAAAGTAAACACTGACTTTTGAAAGCAAG

FIGURE 2

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEYERNIEEMVA
QLRNSSELAQRKCEVNLQLWMSNKRSLS PWGYSINHDP SRIPVDLPEARCLCLGCVNPFTMQEDRSMVSVP
VFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

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GCCAGGTGTGCAGGCCGCTCCAAGCCAGCCTGCCCCGCTGCCGCCACC**ATG**ACGCTCCTCCCCGGCCTCC
TGTTTTCTGACCTGGCTGCACACATGCCTGGCCCCACCATGACCCCTCCCTCAGGGGGCACCCCCACAGTCAC
GGTACCCCACTGCTACTCGGCTGAGGAACTGCCCCTCGGCCAGGCCCCCCCCACACCTGCTGGCTCGAGG
TGCCAAAGTGGGGGCAGGCTTTGCCCTGTAGCCCTGGTGTCCAGCCTGGAGGCAGCAAGCCACAGGGGGAGGC
ACGAGAGGCCCTCAGCTACGACCCAGTGCCCCGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCAC
CAGCGCTCCATCTCACCCCTGGAGATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTT
CGCCGAGTGCCCTGTGCAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGC
GGCTGCTCCAGAGCCTGCTGGTGTGCGCCGCCGGCCCTGCTCCCGCAGCGGCTCGGGGCTCCCCACACCT
GGGGCCTTTGCCCTTCCACACCGAGTTCATCCACGTCCCCGTGCGCTGCACCTGCGTGCTGCCCCGTTCACT
G**TGA**CCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCAGAGGGCACCCCCCTATTTATGTG
TATTTATTGTTATTTATATAGCCTCCCCCAACACTACCCTTGGGGTCTGGGCATTCCCCGTGTCTGGAGGAC
AGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGTTGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGC
CCTTAAAGCTGCAGAAAAGGTGTCACACGGCTGCCTGTACCTTGGCTCCCTGTCTCCTGCTCCCGGCTTCCCT
TACCTTATCACTGGCCTCAGGCCCCGCGAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTA
AACAAATTATTTAAAGTGTACGTGTATTATTAAACTGATGAACACATCCCCAAA

FIGURE 4

MTLLPGLLFLTWLHTCLAHHDPSLRGHPSHGTTPHCYSAEELPLGQAPPHLLARGAKWGQALPVALVSSLE
AASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDED RYPQKLAF AECLCRGCIDARTGRE
TAALNSVRLQLSLLVLRRRPCSRDGSGGLPTPGAF AFHTEFIHVPVGCTCVLPRSV

| | |
|---------------------------------------|------------------------------------|
| Signal peptide: | Amino acids 1-18 |
| Tyrosine kinase phosphorylation site: | Amino acids 112-121 |
| N-myristoylation sites: | Amino acids 32-38;55-61;133-139 |
| Leucine zipper pattern: | Amino acids 3-25 |
| Homologous region to IL-17: | Amino acids 99-195 |

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GGCTTGTCTGAAAAATAAAATCAGGACTCCTAACCTGCTCCAGTCAGCCTGCTTCCACGAGGCCTGTCTAGTCA
GTGCCCCGACTTGTGACTGAGTGTGTCAGTGTCCAGCATGTACAGGTTCAGTGCAGAGGGCTGCCTGAGGGCT
GTGCTGAGAGGGAGAGGAGCAGAGATGCTGCTGAGGGTGGAGGGAGGCCAAGCTGCCAGGTTTGGGGCTGG
GGGCCAAGTGGAGTGAGAACTGGGATCCAGGGGGAGGGTGCAGATGAGGGAGCGACCCAGATTAGGTGA
GGACAGTTCTCTCATTAGCCTTTTCTACAGGTGGTTGCATTCTTGGCAATGGTTCATGGGAACCCACACCT
ACAGCCACTGGCCCAGCTGCTGCCCCAGCAAAGGGCAGGACACCTCTGAGGAGCTGCTGAGGTGGAGCACT
GTGCCTGTGCCTCCCCTAGAGCCTGCTAGGCCCAACCGCCACCCAGAGTCTGTAGGGCCAGTGAAGATGGA
CCCCCTCAACAGCAGGGCCATCTCCCCCTGGAGATATGAGTTGGACAGAGACTTGAAACCGCTCCCCCAGGA
CCTGTACCACGCCCCTTGCTGTGCCCCGACTGCGTCAGCCTACAGACAGGCTCCCATATGGACCCCCGGG
GCAACTCGGAGCTGCTCTACCACAACCAGACTGTCTTCTACAGGCGGCCATGCCATGGCGAGAAGGGCACCC
CACAAGGGCTACTGCCTGGAGCGCAGGCTGTACCGTGTCTTCTTAGCTTGTGTGTGTGTGCGGGCCCCGTGT
GATGGGCTAGCCGGACCTGCTGGAGGCTGGTCCCTTTTGGGAAACCTGGAGCCAGGTGTACAACCACTTG
CCATGAAGGGCCAGGATGCCCAGATGCTTGGCCCCCTGTGAAGTGTCTGTCTGGAGCAGCAGGATCCCGGGAC
AGGATGGGGGGCTTTGGGGAAACCTGCACCTTCTGCACATTTTGAAAAGAGCAGCTGCTGCTTAGGGCCGC
CGGAAGCTGGTGTCTGTCACTTTCTCTCAGGAAAGGTTTTCAAAGTTCTGCCCATTTCTGGAGGCCACCA
CTCCTGTCTCTTCTCTTTTCCCATCCCCTGCTACCCTGGCCCAGCACAGGCACCTTTCTAGATATTTCCCC
CTTGCTGGAGAAGAAAGAGCCCCCTGGTTTTATTTGTTTGTCTTACTCATCACTCAGTGAGCATCTACTTTGG
GTGCATTCTAGTGTAGTTACTAGTCTTTTGACATGGATGATTCTGAGGAGGAAGCTGTTATTGAATGTATA
GAGATTTATCCAAATAAATATCTTTATTTAAAAATGAAAAA

FIGURE 6

MRERPRLGEDSSLISLFLQVVAFLAMVMGTHYSHWPSCCPSKGQDTSEELLRWSTVPVPPLEPARPNRHP
ESCRASEDGPLNSRAISPWRYELDRDLNRLPQDLYHARCLCPHCVSLQTGSHMDPRGNSELLYHNQTVFYR
RPCHGEKGTHKGYCLERRLYRVSLACVCVRPRVMG

Signal peptide: Amino acids 1-32

N-glycosylation site: Amino acids 136-140

Tyrosine kinase phosphorylation site: Amino acids 127-135

N-myristoylation sites: Amino acids 44-50;150-156

205757 2570007

FIGURE 7

ATGCTGGTAGCCGGCTTCCTGCTGGCGCTGCCGCCGAGCTGGGCCGCGGGCGCCCCAGGGCGGGCAGGCG
CCCCGCGCGCCCGCGGGGCTGCGCGGACCGGCCGGAGGAGCTACTGGAGCAGCTGTACGGGCGCCTGGCGG
CCGGCGTGCTCAGTGCCCTTCCACCACACGCTGCAGCTGGGGCCGCGTGAGCAGGCGCGCAACGCGAGCTGC
CCGGCAGGGGGCAGGCCCCGGCGACCGCCGCTTCCGGCCGCCACCAACCTGCGCAGCGTGTGCCCCCTGGGC
CTACAGAATCTCCTACGACCCGGCGAGGTACCCAGGTACCTGCCTGAAGCCTACTGCCTGTGCCGGGGCT
GCCTGACCGGGCTGTTGCGCGAGGAGGACGTGCGCTTCCGCGAGCGCCCCCTGTCTACATGCCCCACCGTCGTC
CTGCGCCGCACCCCGCCTGCGCCGGCGGCCGTTCCGTCTACACCGAGGCCCTACGTCACCATCCCCGTGGG
CTGCACCTGCGTCCCCGAGCCGGAGAAGGACGCAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCCA
AGCTCCTGCTGGGCCCCAACGACGCGCCCGCTGGCCCCCTGAGGCCGCTCCTGCCCCGGGAGGTCTCCCCGG
CCCGCATCCCGAGGCGCCCAAGCTGGAGCCGCTGGAGGGCTCGGTGCGCGACCTCTGAAGAGAGTGACACC
GAGCAAACCAAGTGCCGGAGCACCAGCGCCGCTTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGG
GCATCCCTGGCTTGCTTTTAGCTACAAGCAAGCAGCGTGGCTGGAAGCTGATGGGAAACGACCCGGCACGG
GCATCCTGTGTGCGGCCCGCATGGAGGGTTTGAAAAAGTTCACGGAGGCTCCCTGAGGAGCCTCTCAGATC
GGCTGCTGCGGGTGACGGGCGTGACTCACCGCTGGGTGCTTGCCAAAGAGATAGGGACGCATATGCTTTTT
AAAGCAATCTAAAAATAATAAAGTATAGCGACTATATACCTACTTTTAAATCAACTGTTTTGAATAGA
GGCAGAGCTATTTTATATTATCAAATGAGAGCTACTCTGTTACATTTCTTAACATATAAACATCGTTTTTT
ACTTCTTCTGGTAGAATTTTTTAAAGCATAATTGGAATCCTTGGATAAATTTGTAGCTGGTACACTCTGG
CCTGGGTCTCTGAATTCAGCCTGTCAACGATGGCTGACTGATGAAATGGACACGTCTCATCTGACCCACTC
TTCCTTCCACTGAAGGTCTTCACGGGCCCTCCAGGTGGACCAAAGGGATGCACAGGCGGCTCGCATGCCCCA
GGGCCAGCTAAGAGTTCCAAAGATCTCAGATTTGGTTTTAGTCATGAATACATAAACAGTCTCAAACCTCGC
ACAATTTTTTCCCCCTTTTGAAAGCCACTGGGGCCAATTTGTGGTTAAGAGGTGGTGAGATAAGAAGTGA
ACGTGACATCTTTGCCAGTTGTCAGAAGAATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTTAGGATCA
GGCTGAATATGAGGACAAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTTCTGTTTCTGCA
TTCTGCCACGAGAGCTAGGTCCTTGATCTTTTCTTTAGATTGAAAGTCTGTCTCTGAACACAATTATTTGT
AAAAGTTAGTAGTTCTTTTTTAAATCATTAAAAGAGGCTTGCTGAAGGAT

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FIGURE 8

MLVAGFLLALPPSWAAGAPRAGRPARPRGCADRPEELLEQLYGRLAAGVLSAFHHTLQLGPREQARNASC
PAGGRPGDRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLCRGCLTGLFGCEEDVRFRSAPVYMPTVV
LRRTPACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQAKLLLGPNDAAGP

| | |
|---------------------------------------|---|
| Signal peptide: | Amino acids 1-15 |
| N-glycosylation sites: | Amino acids 68-72;181-185 |
| Tyrosine kinase phosphorylation site: | Amino acids 97-106 |
| N-myristoylation sites: | Amino acids 17-23;49-55;74-80; 118-124 |
| Amidation site: | Amino acids 21-25 |

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FIGURE 9

CAACTGCACCTCGGTTCTATCGATAGCCACCAGCGCAACATGACAGTGAAGACCCTGCATGGCCCAGCCAT
GGTCAAGTACTTGCTGCTGTTCGATATTGGGGCTTGCCTTTCTGAGTGAGGCGGCAGCTCGGAAAATCCCCA
AAGTAGGACATACTTTTTTCCAAAAGCCTGAGAGTTGCCCCGCCTGTGCCAGGAGGTAGTATGAAGCTTGAC
ATTGGCATCATCAATGAAAACCAGCGCGTTTCCATGTCACGTAACATCGAGAGCCGCTCCACCTCCCCCTG
GAATTACACTGTCACTTGGGACCCCCAACCGGTACCCCTCGGAAGTTGTACAGGCCCAGTGTAGGAACTTGG
GCTGCATCAATGCTCAAGGAAAGGAAGACATCTCCATGAATTCCGTTCCCATCCAGCAAGAGACCCTGGTCGTC
CGGAGGAAGCACCAAGGCTGCTCTGTTTCTTTCCAGTTGGAGAAGGTGCTGGTGACTGTTGGCTGCACCTG
CGTCACCCCTGTCATCCACCATGTGCAGTAAGAGGTGCATATCCACTCAGCTGAAGAAG

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FIGURE 10

MTVKTLHGPMVKYLLLSILGLAFLSEAAARKIPKVGHTFFQKPESCPPVPGGSMKLDIGIINENQRVSMS
RNIESRSTSPWNYTWTWDPNRYPSSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVVRRKHQGCSVSFQ
LEKVLVTVGCTCVTPVIHHVQ

Signal sequence:

Amino acids 1-30

N-glycosylation site:

Amino acids 83-86

N-myristoylation sites:

Amino acids 106-111;136-141

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FIGURE 11

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAGCCGACCGT
TCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTAATCCCCGAGAGCTTGA
GGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGACTATTCAATTTTGATGAATGTAAGC
TGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAGGCCACCAAGATTTGTGTGACGGGCAAAAGCAA
CTTCCAGTCTACAGCTGTGTGAGGTGCAATTACACAGAGGCCCTTCCAGACTCAGACCAGACCCTCTGGTG
GTAAATGGACATTTTCTTACATCGGCTTCCCTGTAGAGCTGAACACAGTCTATTTTATTGGGGCCCATAAAT
ATTCTTAATGCAAATATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGA
CCACATAATGAAATATAAAAAAAGTGTGTCAAGGCCGAAGCCTGTGGGATCCGAACATCACTGCTTGTA
AGAAGAATGAGGAGACAGTAGAAGTGAACCTTCAACACCACTCCCCTGGGAAACAGATACATGGCTCTTATC
CAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAACAAACGCGAGCTTCAGT
GGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTGACTCCATATTTTCTACTTGTGGCA
GCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGCCCACAAACAGGCGTCCCTTTCCCTCTGGATAAC
AACAAAAGCAAGCCGGGAGGCTGGCTGCCTCTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGT
GGCAGGGATCTATCTAATGTGGAGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGC
CCCCCATTAAGGTTCTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAA
TTTCTTCAAAACCATTGCAAGTGAAGTCACTCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATGGG
TCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCCAATGACGTCA
ACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAACTCTCAAGACCTCTTCCCC
CTTGCCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCACTGCACAAATACGTGGTGGTCTACTT
TAGAGAGATTGATACAAAAGACGATTACAATGCTCTCAGTGTCTGCCCCAAGTACCACCTCATGAAGGATG
CCACTGCTTTCTGTGCAGAACTTCTCCATGTCAAGCAGCAGGTGTGAGCAGGAAAAAGATCACAAGCCTGC
CACGATGGCTGCTGCTCCTTGTA

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FIGURE 12

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLPGLRDLRVEPVTTSVATGDYSILMNVSWV
LRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGFPVELNTVYFIGAHNIP
NANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKKNEETVEVNFTTTPLGNRYMALIQH
STIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTPYFPTCGSDCIRHKGTVVLCPQTGVFPPLDNNK
SKPGGWLPLLLLSLLVATWVLVAGIYLMWRHERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFL
QNHCRSEVILEKWQKKKIAEMGFPVQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLA
FNLFCSDLRSQIHLHKYVVVYFREIDTKDDYNALSVC PKYHLMKDATAFCAELLHVKKQVSAGKRSQACHD
GCCSL

| | |
|--|---|
| Signal sequence: | Amino acids 1-14 |
| Transmembrane domain: | Amino acids 290-309 |
| N-glycosylation sites: | Amino acids 67-70;103-106;156-159; 183-186;197-200;283-286 |
| cAMP- and cGMP-dependent protein kinase phosphorylation sites: | Amino acids 228-231;319-322 |
| N-myristoylation site: | Amino acids 116-121 |
| Amidation site: | Amino acids 488-491 |

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FIGURE 13

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCAGGACAGAG
AGTGACAAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGGATTCCAGCCCCTGCCA
CCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGGAGCACAGGGCCTCAGGCCTGGGT
GCCACCTGGCACCTAGAAGATGCTGTGCCCTGGTTCTTGCTGTCTTGGCACTGGGCCGAAGCCCAGTGG
TCCTTTCTCTGGAGAGGCTTGTGGGGCCTCAGGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTC
TGGGACAGTGACATACTCTGCCTGCCTGGGGACATCGTGCCGTCTCCGGGCCCCGTGCTGGCGCCTACGCA
CCTGCAGACAGAGCTGGTGTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCC
ACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGGG
GTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCTTACTGCCCG
CTGCGTCTGTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTCTGTGGGCTCTGTGGTATAT
GACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTCCTATACTCAGCCCAGGTACGAGAAGGA
ACTCAACCACACAGCAGCTGCCTGCCCTGCCCTGGCTCAACGTGTGAGCAGATGGTGACAACGTGCATC
TGTTTCTGAATGTCTCTGAGGAGCAGCACTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCA
AAACCCCGGTGGCACAAAAACCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTG
CCTCTGTATTAGGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCTTCAGGGAGGACC
CCCGCGCACACCAGAACCTCTGGCAAGCCGCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCTGGAC
GCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCCCTGCCAGCCACT
GGTCCCACCGCTTTCTCTGGGAGAAGCTCACTGTGGACAAGGTTCTCGAGTTCCCATTTGCTGAAAGGCCACC
CTAACCTCTGTGTTAGGTGAACAGCTCGGAGAAGCTGCAGCTGCAGGAGTGCTTGTGGGCTGACTCCCTG
GGGCCTCTCAAAGACGATGTGCTACTGTTGGAGACACGAGGCCCCAGGACAACAGATCCCTCTGTGCCTT
GGAACCCAGTGGCTGTACTTCACTACCCAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTAC
TACAAGACCTGCAGTCAGGCCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCC
ATGGACAAATACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTC
CCTCATCTCTCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCGCTCGG
GGGCGGCCCGCCAGGGGCCGCGGGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTTCGAGCGCCTGGTG
GGCGCCCTGGCGTCCGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGACCTGTGGAGCCGTGCTGAAC
GAGCGCGCAGGGGCCCGTGGCTTGGTTTACGCGCAGCGGCCAGACCCTGCAGGAGGGCGGCGTGGTGG
TCTTGCTCTTCTCTCCCGTGGGTGGCGCTGTGCAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCGGG
GCGCACGGCCCGCACGACGCTTCCGCGCCTCGCTCAGCTGCGTGCTGCCCGACTTCTTGAGGGCCGGGC
GCCCGGCAGCTACGTGGGGGCTGCTTCGACAGGCTGCTCCACCCGACGCGGTACCCGCCCTTTTCCGCA
CCGTGCCCGTCTTACACTGCCCTCCCAACTGCCAGACTTCTTGGGGGCCCTGCAGCAGCCTCGCGCCCCG
CGTTCGGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTACCCAGCCCTGGATAGCTACTT
CCATCCCCCGGGACTCCCGCGCGGGGACGCGGGGTGGGACCAGGGGCGGGACCTGGGGCGGGGACGGGA
CTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

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FIGURE 14

MPVPWFLLSLALGRSPVVLSELRLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAPGPFVLAPTHLQTELV
LRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRNASLQAQVVLSFQAYPTARCVLLEV
QVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYTQPRYEKELNHTQQLPALPWLNVSAADGNVHLVLNV
EEQHFGLSLYWNQVQGGPKPRWHKNLTGPQIITLNTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQ
LWQAARLRLTLQSWLLDAPCSLPAAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCVQ
VNSSEKLQEQECLWADSLGPKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRAARLGEYLLQDLQS
GQCLQLWDDDLGALWACPMKYIHKRWLVWLACLLFAAALSLILLKKDHAKGWLRLKQDVRSAAAARG
RAALLYSADDSGFERLVGALASALCQLPLRVAVDLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSP
GAVALCSEWLQDGVSGPAHGPHDAFRASLSCVLPDFLQGRAPGSYVGACFDRLHLPDAVPALFRTVPVFT
LPSQLPDFLQALQPRAPRSGRLQERAEQVSRLQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT

| | |
|---|---|
| signal sequence: | Amino acids 1-20 |
| transmembrane domain: | Amino acids 453-473 |
| N-glycosylation sites: | Amino acids 118-121;186-189;198-201; 211-214;238-241;248-251;334-337; 357-360;391-394 |
| Glycosaminoglycan attachment site: | Amino acids 583-586 |
| cAMP- and cGMP-dependent protein kinase phosphorylation site: | Amino acids 552-555 |
| N-myristoylation sites: | Amino acids 107-112;152-157;319-324; 438-443;516-521;612-617;692-697; 696-701;700-705 |

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FIGURE 15

CGAGGGCTCCTGCTGGTACTGTGTTGCTGCTGCACAGCAAGGCCCTGCCACCCACCTTCAGGCCATGCAG
CCATGTTCCGGGAGCCCTAATTGCACAGAAGCCCATGGGGAGCTCCAGACTGGCAGCCCTGCTCCTGCCTC
TCCTCCTCATAGTCATCGACCTCTCTGACTCTGCTGGGATTGGCTTTCGCCACCTGCCCCACTGGAACACC
CGCTGTCTCTGGCCTCCACACGGATGACAGTTTCACTGGAAGTTCTGCCTATATCCCTTGCCGCACCTG
GTGGGCCCTCTTCTCCACAAAGCCTTGGTGTGTGCGAGTCTGGCACTGTTCGCTGTTTGTGCCAGCATCTGC
TGTCAAGTGGCTCAGGTCTTCAACGGGGCCTCTTCCACCTCCTGGTGCAGAAATCCAAAAGTCTTCCACA
TTCAAGTTCATAGGAGACACAAGATGCCAGCACCTGCTCAGAGGAAGCTGCTGCCTCGTCGTACCTGTCTC
TGAGAAGAGCCATCACATTTCCATCCCCTCCCCAGACATCTCCACAAGGGACTTCGCTCTAAAAGGACCC
AACCTTCGGATCCAGAGACATGGGAAAGTCTTCCCAGATTGGACTCACAAGGCATGGAGGACCCGAGTTC
TCCTTTGATTTGCTGCCTGAGGCCCGGGCTATTCCGGGTGACCATATCTTCAGGCCCTGAGGTGAGCGTGCG
TCTTTGTACACAGTGGGCACTGGAGTGTGAAGAGCTGAGCAGTCCCTATGATGTCCAGAAAATTGTGTCTG
GGGGCCACACTGTAGAGCTGCCTTATGAATTCTTCTGCCCTGTCTGTGCATAGAGGCATCCTACCTGCAA
GAGGACACTGTGAGGCGCAAAAAATGTCCCTTCCAGAGCTGGCCAGAAGCCTATGGCTCGGACTTCTGGAA
GTCAGTGCACCTTCACTGACTACAGCCAGCACACTCAGATGGTCATGGCCCTGACACTCCGCTGCCCCTGA
AGCTGGAAGCTGCCCTCTGCCAGAGGCACGACTGGCATACCCCTTTGCAAAGACCTCCCGAATGCCACGGCT
CGAGAGTCAGATGGGTGGTATGTTTTGGAGAAGGTGGACCTGCACCCCCAGCTCTGCTTCAAGTTCCTTT
TGGAACAGCAGCCATGTTGAATGCCCCCACCAGACTGGGTCTCTCACATCCTGGAATGTAAGCATGGATA
CCCAAGCCCAGCAGCTGATTCTTCACTTCTCCTCAAGAATGCATGCCACCTTCAGTGTCTGCCTGGAGCCTC
CCAGGCTTGGGGCAGGACACTTTGGTGCCCCCGGTGTACACTGTGAGCCAGGCCCGGGGCTCAAGCCCAGT
GTCAC TAGACCTCATCATTCCTTCTGAGGCCAGGGTGTGTCTGCTGGTGTGGCGGTGAGATGTCCAGT
TTGCCTGGAAGCACCTCTTGTGTCCAGATGTCTCTTACAGACACCTGGGGCTCTTGATCCTGGCACTGCTG
GCCCTCCTCACCTACTGGGTGTTGTTCTGGCCCTCACCTGCCGGCGCCACAGTCAGGCCCGGGGCCAGC
GCGGCCAGTGTCTCTCTGCACGCGGCGGACTCGGAGGCGCAGCGGCGCCTGGTGGGAGCGCTGGCTGAAC
TGCTACGGGCAGCGCTGGGCGGCGGCGGCGACGTGATCGTGGACCTGTGGGAGGGGAGGCACGTGGCGCGCGT
GGGCCCCTGCGGTGGCTCTGGGCGGCGGCGGACGCGCGTAGCGCGGGAGCAGGGCACTGTGCTGCTGCTGT
GGAGCGGCGCGGACCTTCGCCCCGTGAGCGGCCCGACCCCCGCGCGCGCCCCCTGCTCGCCCTGCTCCAC
GCTGCCCCGCGCCGCTGCTGCTGCTGCTTACTTCAGTCGCCTCTGCGCCAAGGGCGACATCCCCCGCC
GCTGCGCGCCCTGCCGCGTACCGCCTGCTGCGCGACCTGCCCGTCTGCTGCGGGCGCTGGACGCGCGGC
CTTTCGCAGAGGCCACCAGCTGGGGCCGCTTGGGGCGCGGCAGCGCAGGCAGAGCCGCTAGAGCTGTGC
AGCCGGCTTGAACGAGAGGCCCGCCGACTTGCAGACCTAGGTTGAGCAGAGCTCCACCGCAGTCCCGGTGTCT

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FIGURE 16

MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTRCPLASHTDDSFSGSSAYIPCRTWWALFSTKPWCV
RVWHCSRCLCQHLLSGGSLQRLFLHLLVQSKKSSTFKFYRRHKMPAPAQRKLLPRRHLSEKSHHISIPS
PDISHKGLRSKRTQPSDPETWESLPRLDSQRHGGPEFSFDLLPEARAIRVTISSGPEVSVRLCHQWALECE
ELSSPYDVQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPFQSWPEAYGSDFWKSVHFTDYSQH
TQMVMALTLCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKFSFGNSSHVECPH
QTGSLTSWNVSMDTQAQQLILHFSSRMHATFSAAWSLPGLGQDTLVPPVYTVSQARGSSPVSLDLIIPFLR
PGCCVLVWRSDVQFAWKHLCPDVSYRHLGLLILALLALLTLLGVVLALTCRRPQSGPGPARPVLLLHAAD
SEAQRRLVGALAEELLRAALGGGRDVIVDLWEGRHVARVGPLPWLWAARTRVAREQGTVLLWLGADLRPV
GPDPRAPLLALLHAAPRPLLLLAYFSRLCAKGDIPPLRALPRYRLRLDLPRLLRALDARPF AEATSWGR
L GARQRRQSRLELCSRLEREAARLADLG

Signal peptide: Amino acids 1-23

Transmembrane domain: Amino acids 455-472

N-glycosylation sites: Amino acids 318-322;347-351;364-368

Glycosaminoglycan attachment site: Amino acids 482-486

cAMP- and cGMP-dependent protein kinase phosphorylation sites:
Amino acids 104-108;645-649

Tyrosine kinase phosphorylation site: Amino acids 322-329

N-myristoylation sites: Amino acids 90-96;358-364;470-476

Eukaryotic cobalamin-binding proteins: Amino acids 453-462

FIGURE 17

GCCAGGCCCTATCTCCCTGCCAGGAGGCCGAGTGGGGGAGGTCAGACGGGGCGGTGGAGGGGGAGGGAT
 GCCACGCGCTTCTGCCTCAGGTGTTCTGCGTTGTTTGTCACTGGAGAGCAGGGAGTGGGGCCAGCCAGCA
 GAAACAGTGGGCTGTACAACATCACCTTCAAATATGACAATTGTACCACCTACTTGAATCCAGTGGGAAG
 CATGTGATTGCTGACGCCCAGAATATCACCATCAGCCAGTATGCTTGCCATGACCAAGTGGCAGTCACCAT
 TCTTTGGTCCCCAGGGGCCCTCGGCATCGAATTCCTGAAAGGATTTCTGGGTAATACTGGAGGAGCTGAAGT
 CGGAGGGAAGACAGTGCCAACAACTGATTCTAAAGGATCCGAAGCAGCTCAACAGTAGCTTCAAAGAAGT
 GGAATGGAATCTCAACCTTTCCTGAATATGAAATTTGAAACGGATTATTTCTGTAAGGTTGTCCCTTTTCC
 TTCCATTAAAAACGAAAGCAATTACCACCTTTCTTCTTTAGAACCCGAGCCTGTGACCTGTTGTTACAGC
 CGGACAATCTAGCTTGTAACCTTCTGGAAGCCTCGGAACCTGAACATCAGCCAGCATGGCTCGGACATGC
 AGGTGTCCTTCGACCACGCACCGCATGGCTCGGACATGCAGGTGTCCTTCGACCACGCACCGCACAACTTC
 GGCTTCCGTTTCTTCTATCTTCACTACAAGCTCAAGCACGAAGGACCTTTCAGCGAAAGACCTGTAAGCA
 GGAGCAAACCTACAGAGATGACCAGCTGCCTCCTTCAAATGTTTCTCCAGGGGATTATATAATTGAGCTGG
 TGGATGACACTAACACAACAAGAAAAGTGATGCATTATGCCTTAAAGCCAGTGCACTCCCCGTGGGCCGGG
 CCCATCAGAGCCGTGGCCATCACAGTGCCACTGGTAGTCATATCGGCATTCTCGGACGCTCTTCACTGTGAT
 GTGCCGCAAGAAGCAACAAGAAAATATATATTACATTTAGATGAAGAGAGCTCTGAGTCTTCCACATACA
 CTGCAGCACTCCCAAGAGAGAGGCTCCGGCCCGGGCCGAAGGTCTTTCTCTGCTATTCCAGTAAAGATGGC
 CAGAATCACATGAATGTCGTCCAGTGTTCGCTACTTCTCCAGGACTTCTGTGGCTGTGAGGTGGCTCT
 GGACCTGTGGGAAGACTTCAGCCTCTGTAGAGAAGGGCAGAGAGAATGGGTATCCAGAAGATCCACGAGT
 CCCAGTTCATCATTTGTGGTTTGTTCCAAAGGTATGAAGTACTTTGTGGACAAGAAGAACTACAAACACAAA
 GGAGGTGGCCGAGGCTCGGGGAAAGGAGAGCTTCTCTGGTGGCGGTGTCAGCCATTGCCGAAAAGCTCCG
 CCAGGCCAAGCAGAGTTCGTCCGCGGCGCTCAGCAAGTTTATCGCCGTCTACTTTGATTATTCTGCGAGG
 GAGACGTCCCCGGTATCCTAGACCTGAGTACCAAGTACAGACTCATGGACAATCTTCTCAGCTCTGTTCC
 CACCTGCACCTCCCGAGACCACGGCCTCCAGGAGCCGGGGCAGCACACGCGACAGGGCAGCAGAAGGAACCTA
 CTTCCGGAGCAAGTCAGGCCGGTCCCTATACGTGCGCATTTGCAACATGCACCAGTTTATTGACGAGGAGC
 CCGACTGGTTTCGAAAAGCAGTTCGTTCCCTTCCATCCTCCTCCACTGCGCTACCGGGAGCCAGTCTTGGAG
 AAATTTGATTTCGGGCTTGGTTTAAATGATGTCATGTGCAAACAGGGCCTGAGAGTGACTTCTGCCTAAA
 GGTAGAGGCGGCTGTTCTTGGGGCAACCGGACCAGCCGACTCCCAGCACGAGAGTCAGCATGGGGGCCCTGG
 ACCAAGACGGGGAGGCCCGGCTGCCCTTGACGGTAGCGCCGCCCTGCAACCCCTGCTGCACACGGTGAAA
 GCCGGCAGCCCCTCGGACATGCCGCGGGACTCAGGCATCTATGACTCGTCTGTGCCCTCATCCGAGCTGTC
 TCTGCCACTGATGGAAGGACTCTCGACGGACCAGACAGAAACGTCTTCCCTGACGGAGAGCGTGTCTCCT
 CTTCAGGCCTGGGTGAGGAGGAACCTCCTGCCCTTCTTCCAAGCTCCTCTCTTCTGGGTGATGCAAAGCA
 GATCTTGGTTGCCGAGCTACACTGATGAACTCCACGCGGTGCGCCCTTTGTAACAAAACGAAAGAGTCTA
 AGCATTGCCACTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 18

MPRASASGVPALFVSGEQGVGPASRNSGLYNITFKYDNCTTYLNPVGKHVIADAQNITISQYACHDQVAVT
ILWSPGALGIEFLKGFRVILEELKSEGRQCQQLILKDPKQLNSSFKRTGMESQPFLNMKFETDYFVKVVPF
PSIKNESNYHPFFFRTRACDLLLQPDNLACKPFWKPRNLNISQHGSDMQVSFDHAPHGSDMQVSFDHAPHN
FGFRFFYLHYKLKHEGPFKRKTCKQEQTTEMTSCLLQNVSPGDYIIELVDDTNTTRKVMHYALKPVHSPWA
GPIRAVAITVPLVVISAFATLFTVMCRKKQQENIYSHLDEESSESSTYTAALPRERLRPRPKVFLCYSSKD
GQNHMNVVQCFAYFLQDFCGCEVALDLWEDFSLCREGQREWVIQKIHESQFIIVVCSKGMKYFVDKKNYKH
KGGGRGSGKGELFLVAVSAIAEKLQAKQSSSAALSKFIAVYFDYSCEGDVPGILDSTKYRLMDNLPQLC
SHLHSRDHGLQEPGQHTROGSRNRYFRSKSGRSLYVAICNMHQFIDEEPWFQFVFPFHPPLRYREPVL
EKFDSGLVLNDVMCKPGPESDFCLKVEAAVLGATGPADSQHESQHGGGLDQDGEARPALDGSAAALQPLLHTV
KAGSPSDMPRDSGIYDSSVPSSSELSLPLMEGLSTDQTETSSLTESVSSSSGLGEEEPALPSKLLSSGSK
ADLGCRSYTDELHAVAPL

Transmembrane domain:

Amino acids 283-307

N-glycosylation sites:

Amino acids 31-34;38-41;56-59;
113-116;147-150;182-185;266-269

Glycosaminoglycan attachment sites: Amino acids 433-436;689-692

cAMP- and cGMP-dependent protein kinase phosphorylation:

Amino acids 232-235

Tyrosine kinase phosphorylation sites:

Amino acids 312-319;416-424

N-myristoylation site:

Amino acids 19-24;375-380;428-433;
429-434;432-437;517-522;574-579;
652-657;707-712

10000157-034500

h-IL17
h-IL17B
h-IL17C
h-IL17D
h-IL17E
h-IL17F

[illegible]

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 66 | Y | Y | N | R | S | T | S | P | W | N | L | H | R | N | E | D | P | E | R | Y | P | S | V | I | W | E | A | K | R | H | L | G | C | I | N | A | D | - | G | N | V | D | Y | H | M | N | S | V | P | |
| 93 | S | N | K | R | S | L | S | P | W | G | Y | S | I | N | H | D | P | S | R | I | P | V | D | L | P | E | A | R | C | L | C | L | G | V | N | P | F | T | M | Q | E | D | R | S | M | V | S | V | P | |
| 101 | T | H | Q | R | S | I | S | P | W | R | Y | R | V | D | T | D | E | D | R | Y | P | Q | K | L | A | F | A | E | C | L | C | R | G | C | I | D | A | R | T | G | R | E | T | A | L | N | S | V | R | |
| 86 | T | N | L | R | S | V | S | P | W | A | Y | R | I | S | Y | D | P | A | R | Y | P | R | Y | L | P | E | A | Y | C | L | C | R | G | C | L | T | G | L | F | G | E | E | D | V | R | F | R | S | A | P |
| 82 | L | N | S | R | A | I | S | P | W | R | Y | E | L | D | R | D | L | N | R | L | P | Q | D | L | Y | H | A | R | C | L | C | P | H | C | V | S | L | Q | T | G | S | H | M | D | P | R | G | N | S | E |
| 74 | I | E | S | R | S | T | S | P | W | N | Y | T | V | T | W | D | P | N | R | Y | P | S | E | V | V | Q | A | Q | C | R | N | L | G | C | I | N | A | Q | - | G | K | E | I | S | M | N | S | V | P | |

h-IL17 115 I Q E I L V L R R E - - - - - P P H C P N S F R L E K I L V S V G C T C V T P I V H H V A

h-IL17B 143 V F S Q V P V R R R L C P P P - - - - - P R T G P C R Q R A V M E T I A V G C T C I F - - - - -

h-IL17C 151 L L Q Q S L L V L R R R P C S R D G S G L P T P G A F A F H T E F I H V P V G C T C V L P R S V - - - - -

h-IL17D 136 V Y M P T V L R R T P A C A G - - - - - G R S V Y T E A Y V T I P V G C T C V P E P E K D A D

h-IL17E 132 L L Y H N Q T V F Y R R P C H G E K - - G T H K G Y C L E R R L Y R V S L A C V C V R P R V M G - - - - -

h-IL17F 123 I Q Q E T L V V R R K - - - - - H Q G C S V S F Q L E K V L V T V G C T C V T P V I H H V Q

h-IL17D 179 S I N S S I D K Q G A K L L L G P N D A P A G P X

FIG. 19

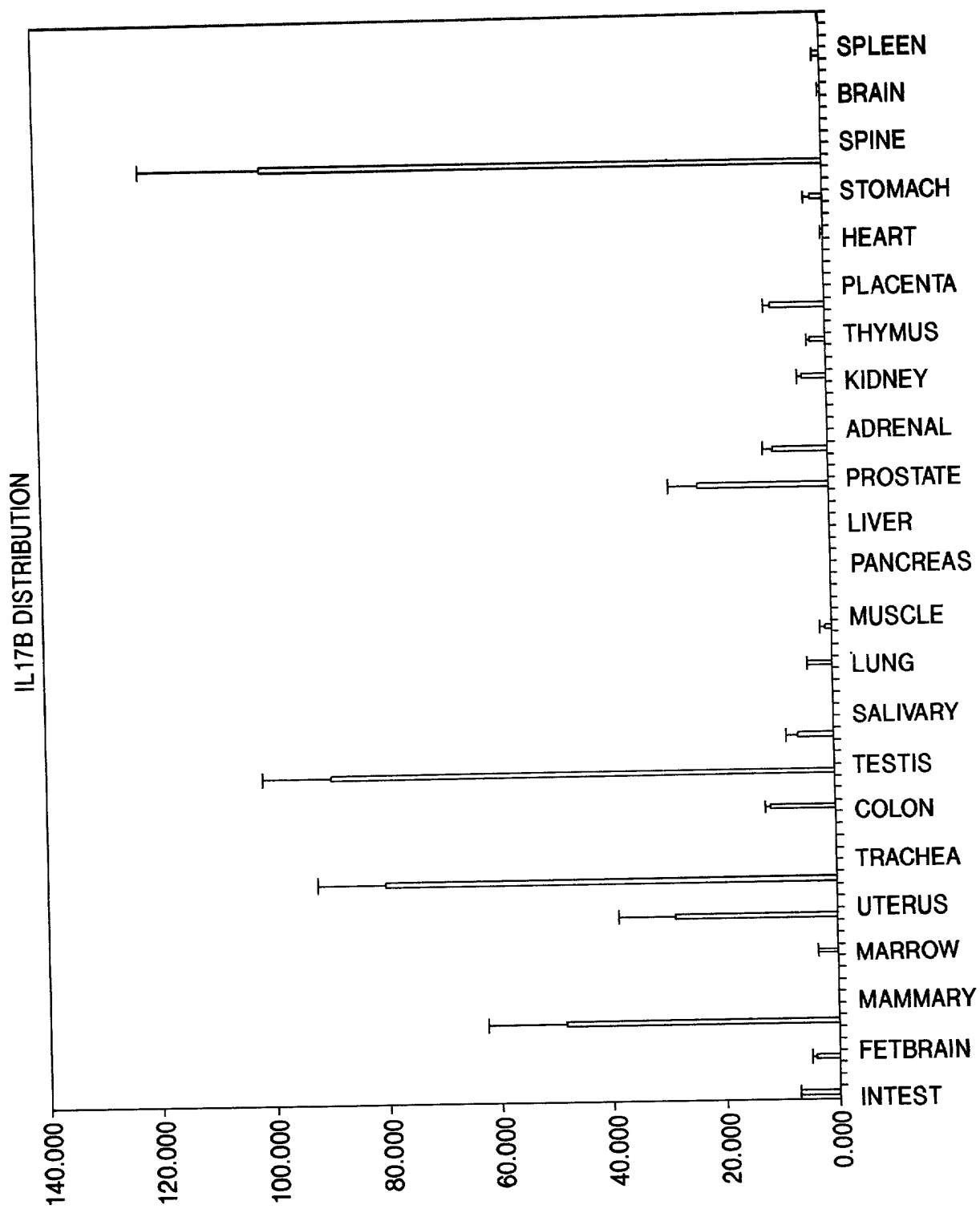


FIG. 20

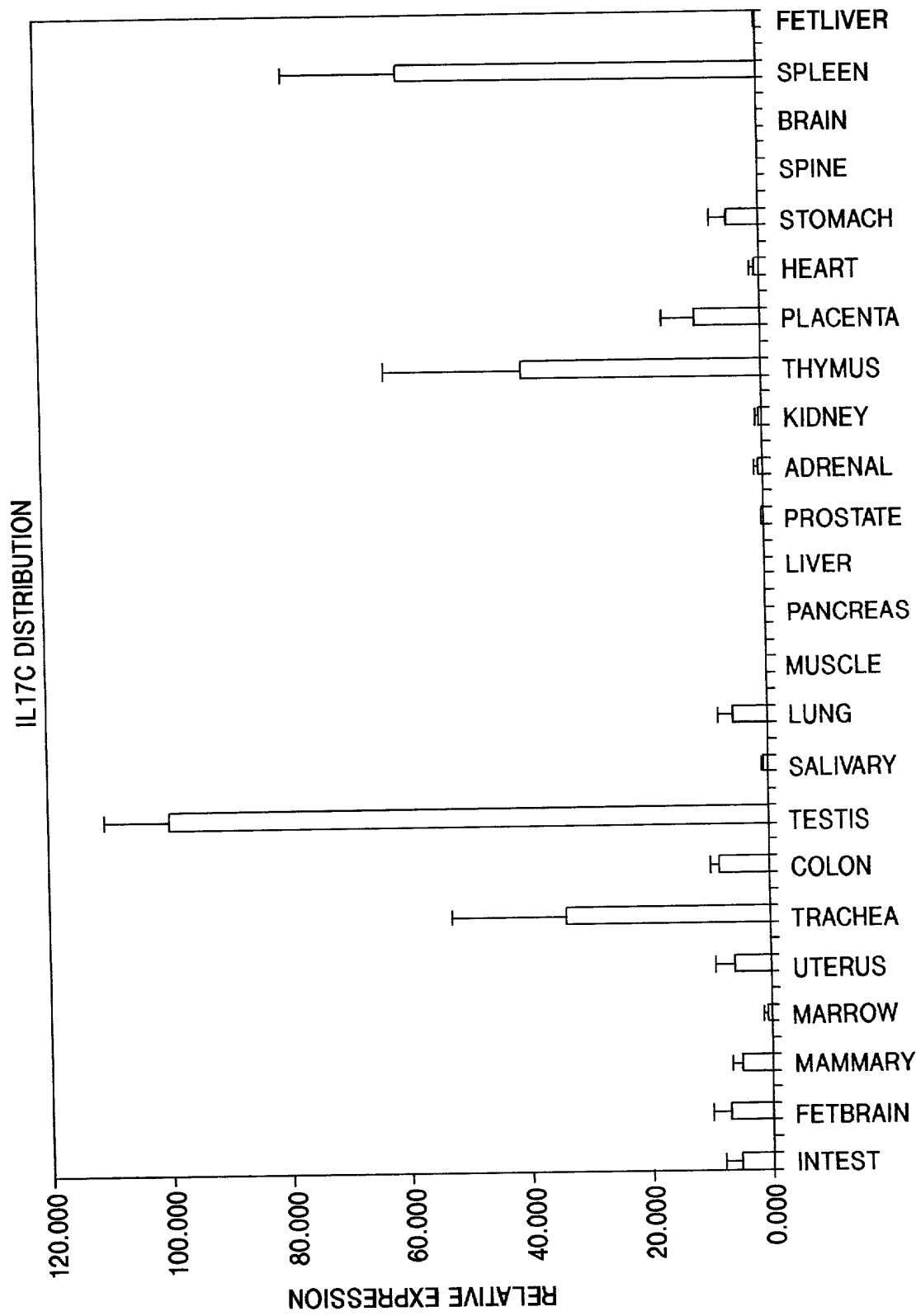


FIG. 21

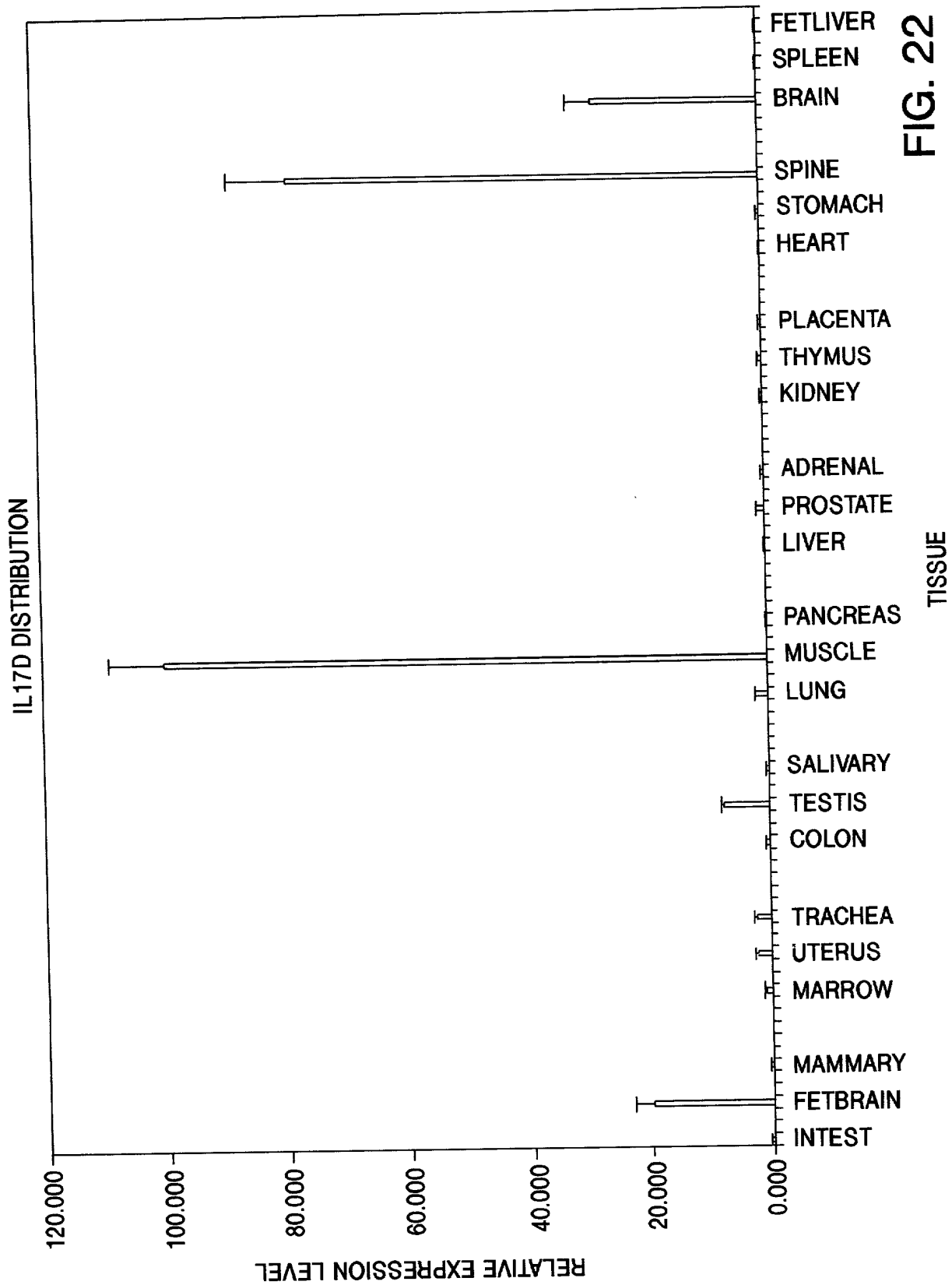


FIG. 22

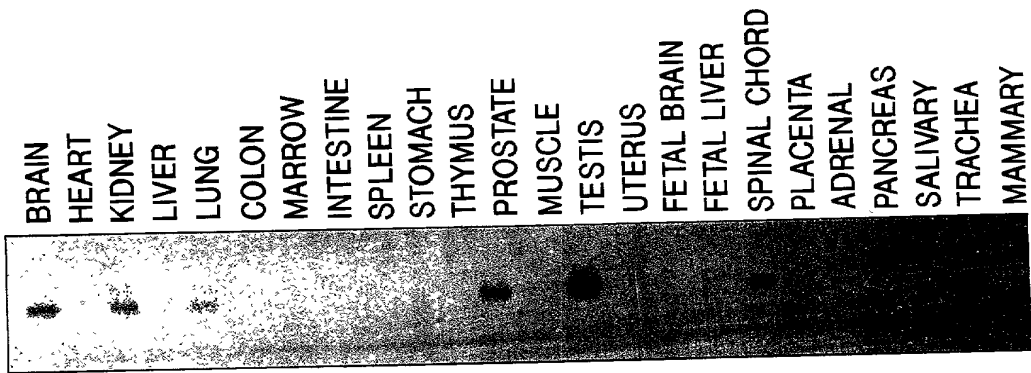


FIG. 23

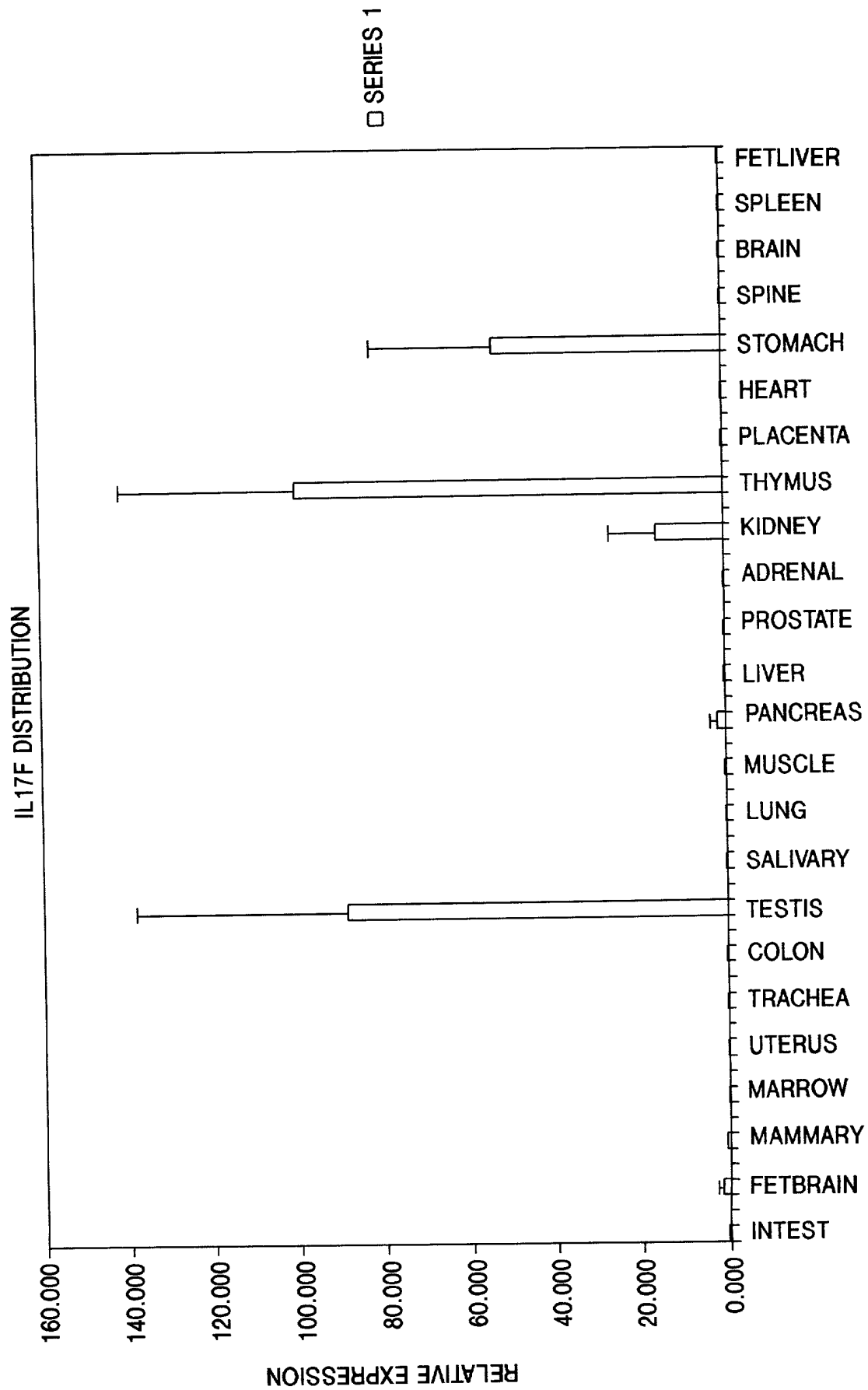


FIG. 24

209769 2510093

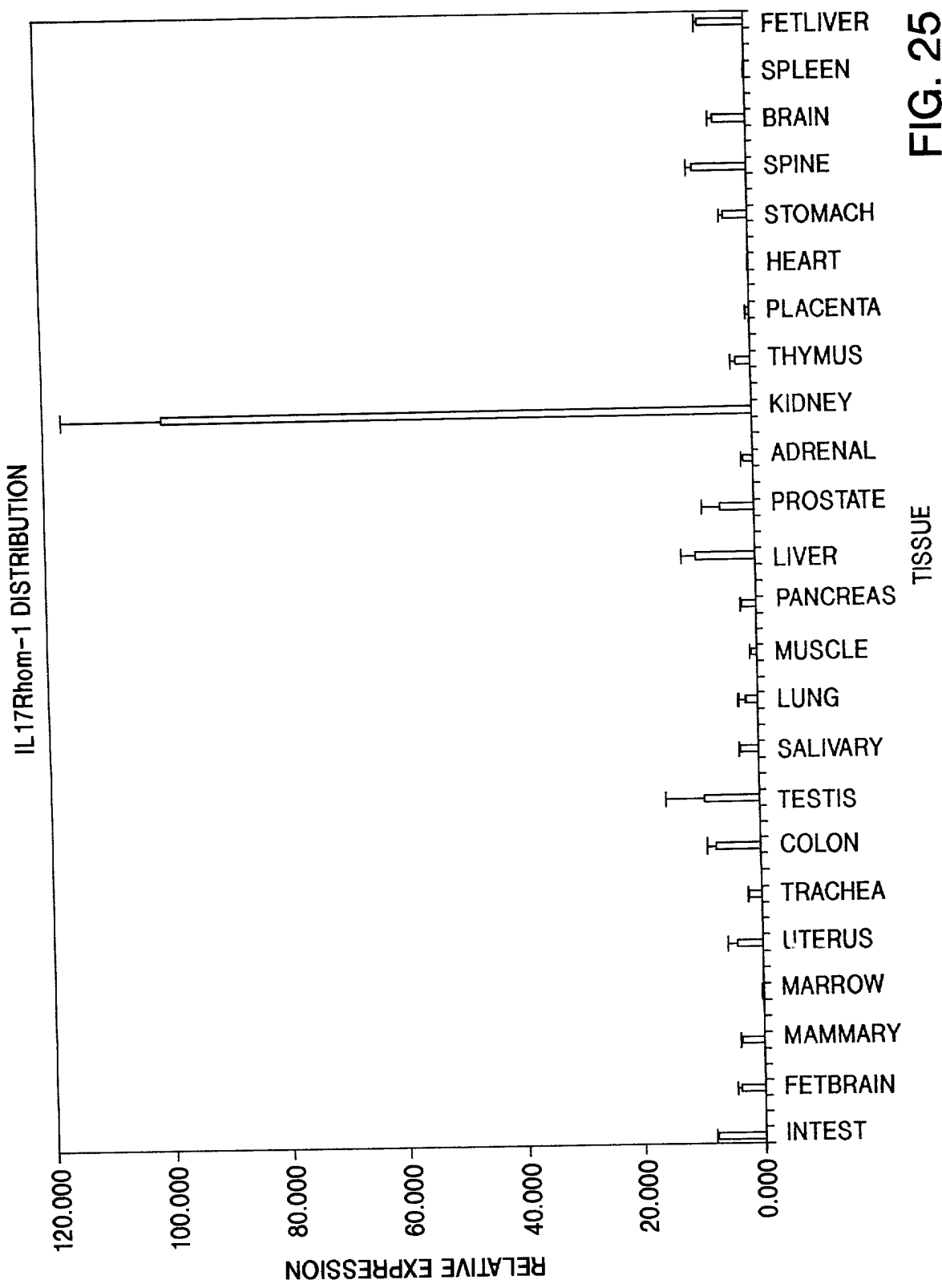


FIG. 25

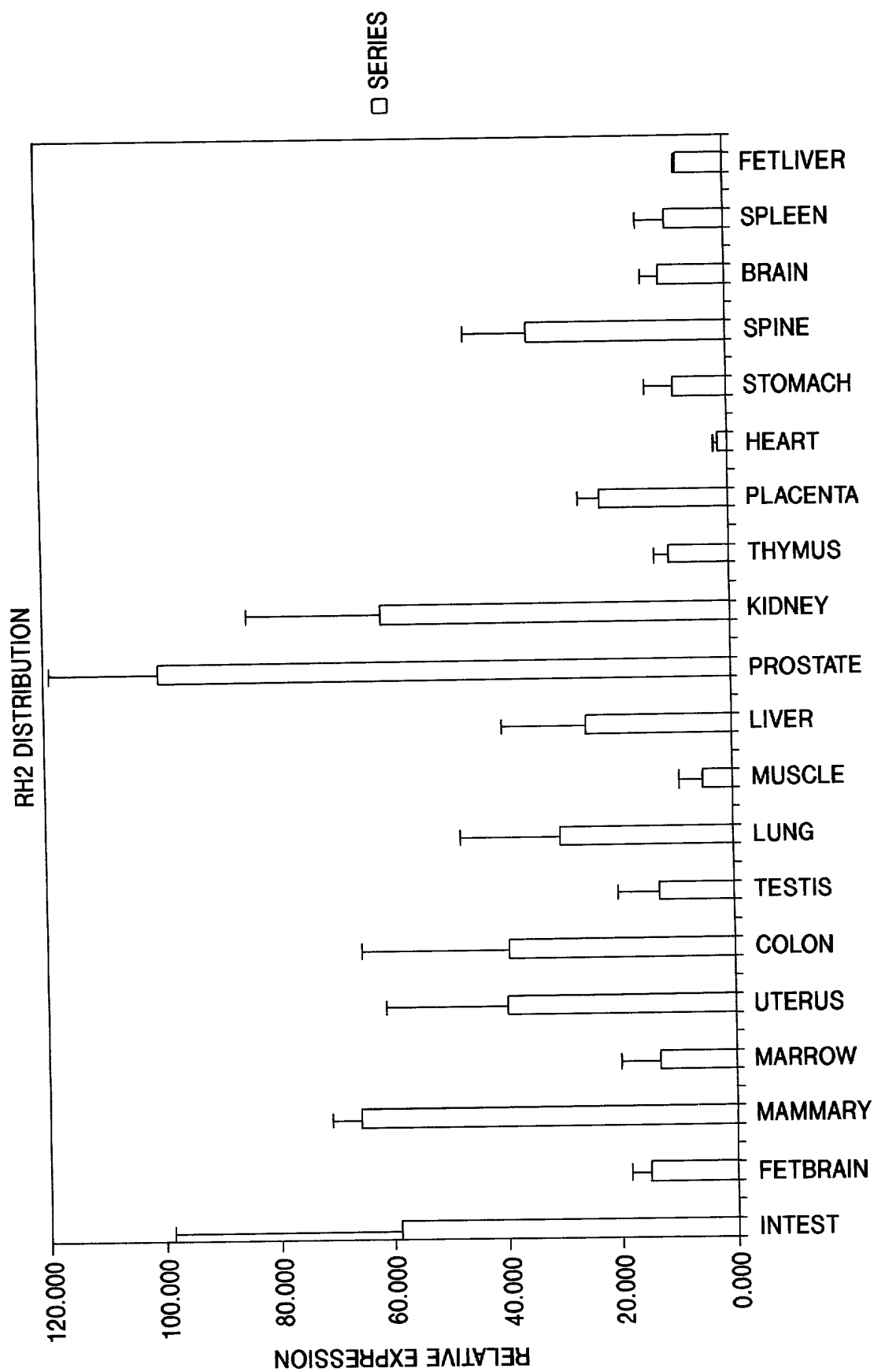


FIG. 26

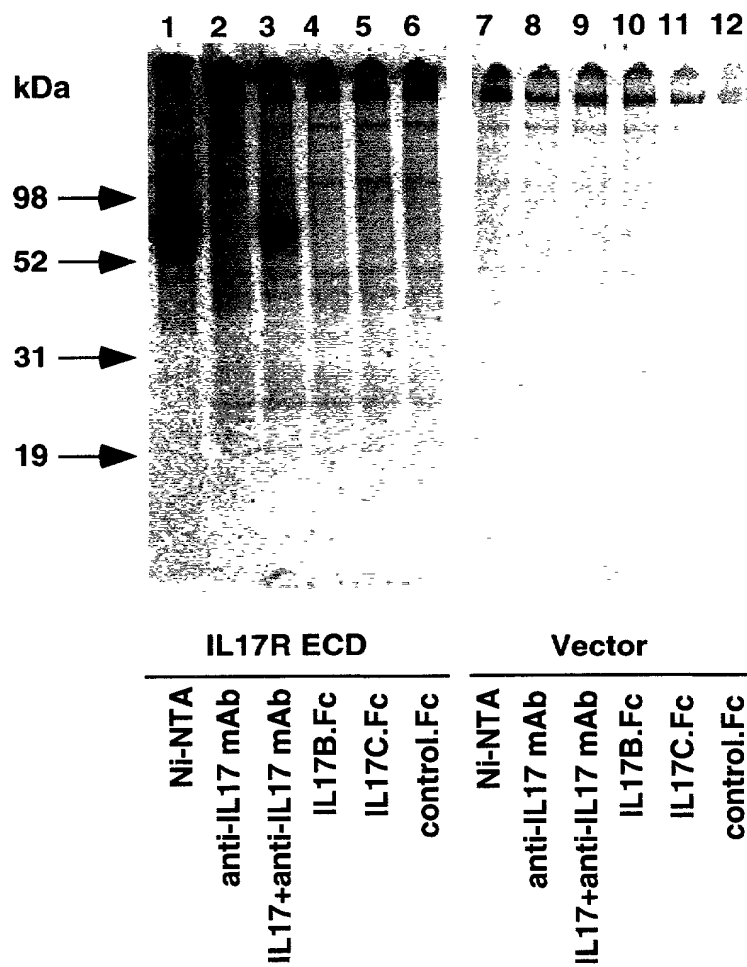


FIG. 29A

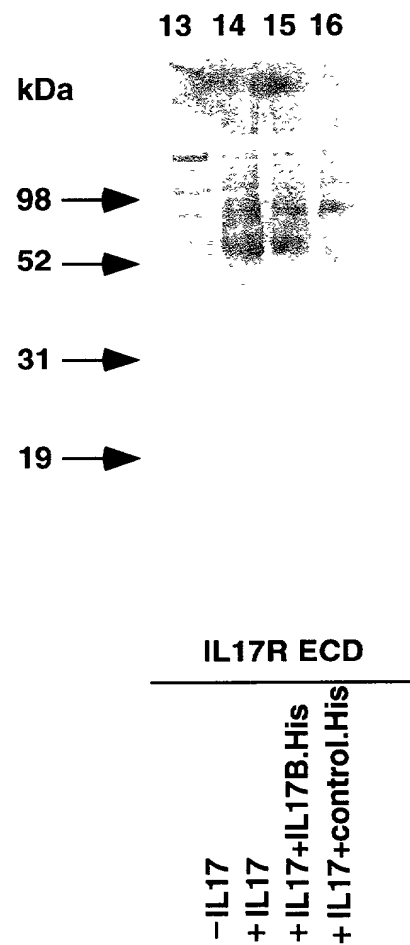


FIG. 29B

FIG. 30

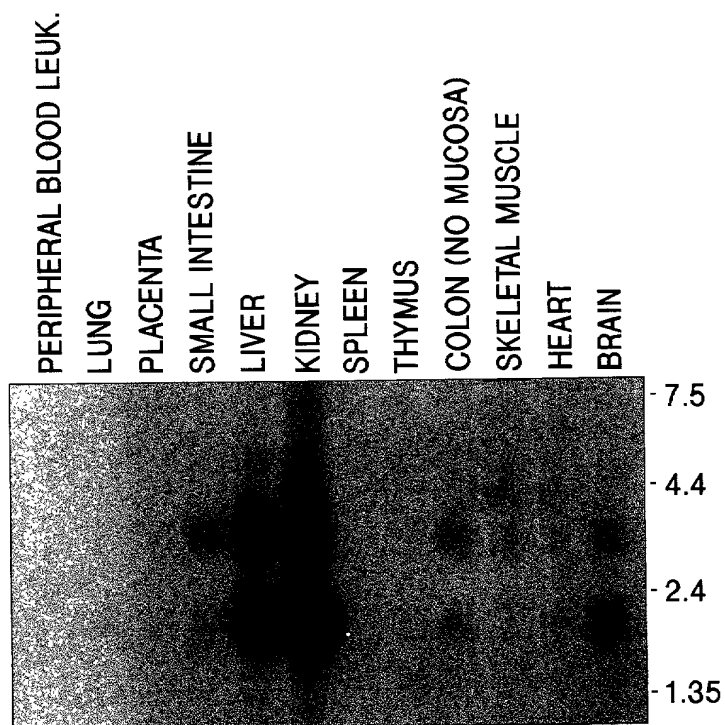


FIG. 31A

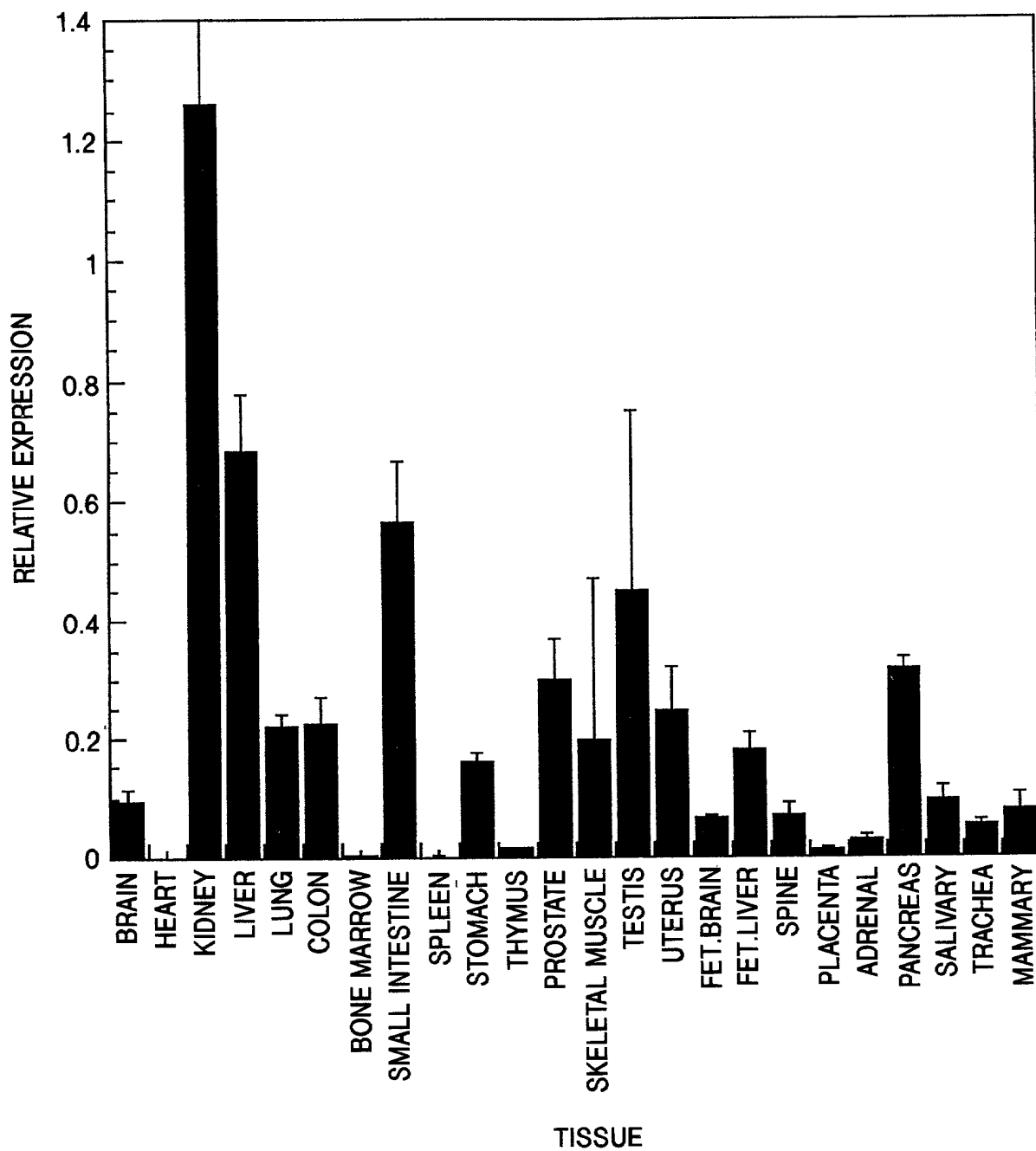


FIG. 31B

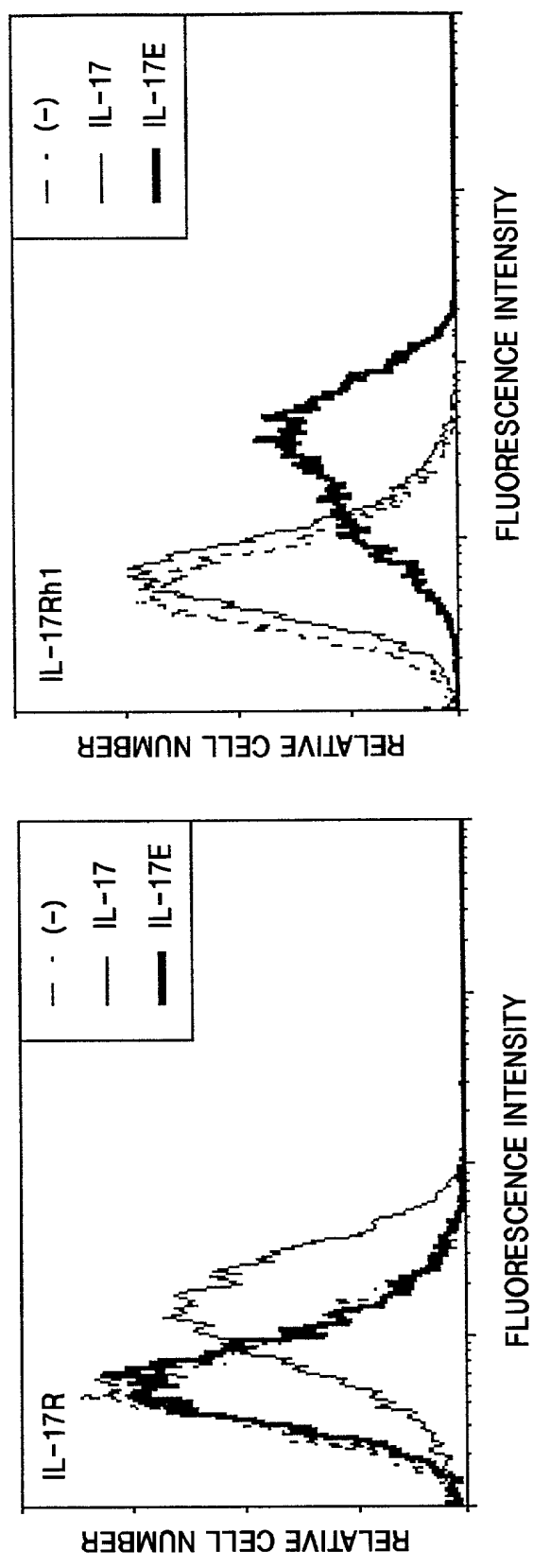


FIG. 32A

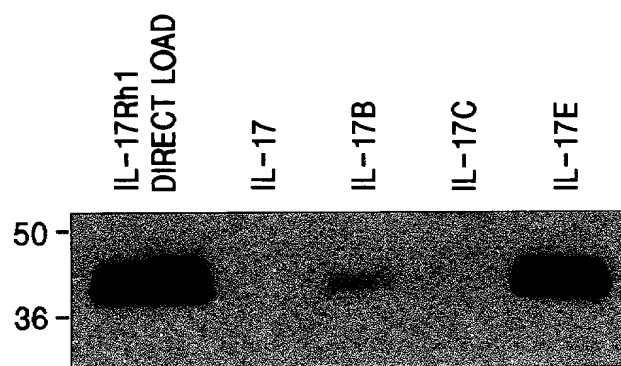


FIG. 32B

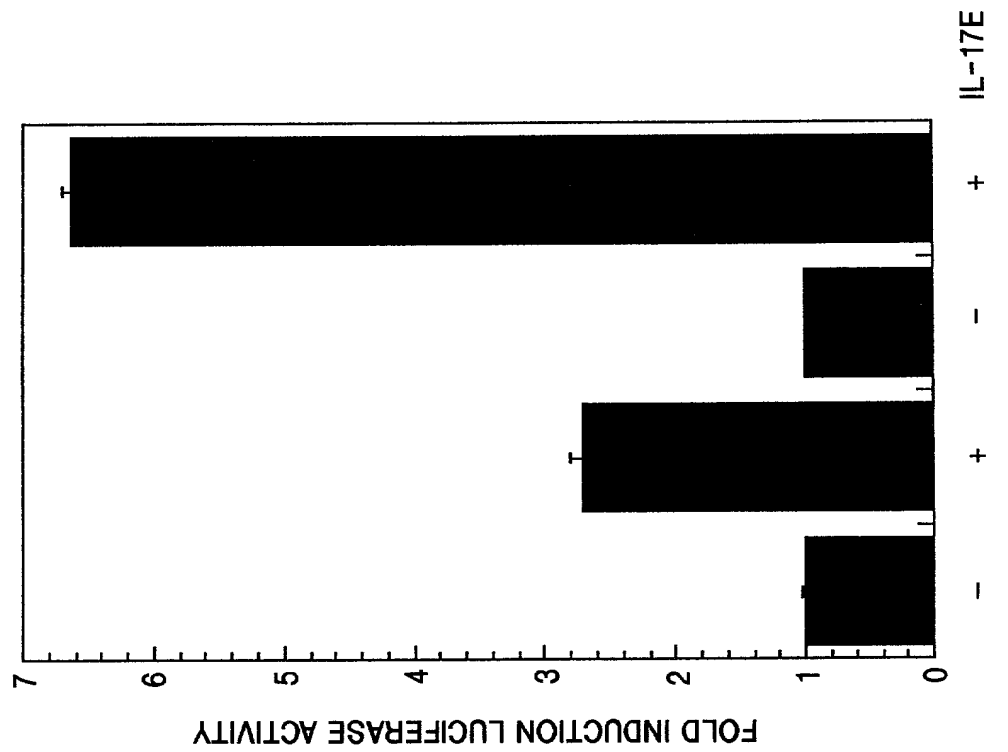


FIG. 33A

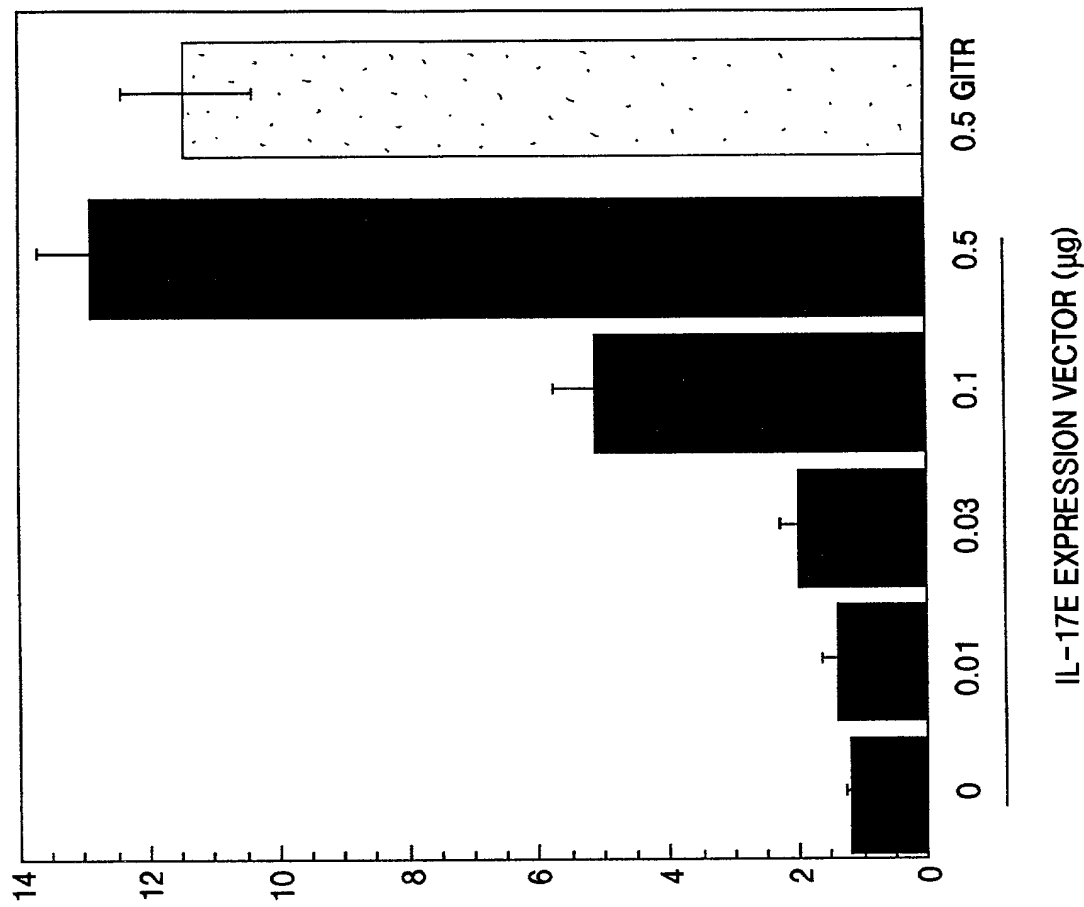


FIG. 33B

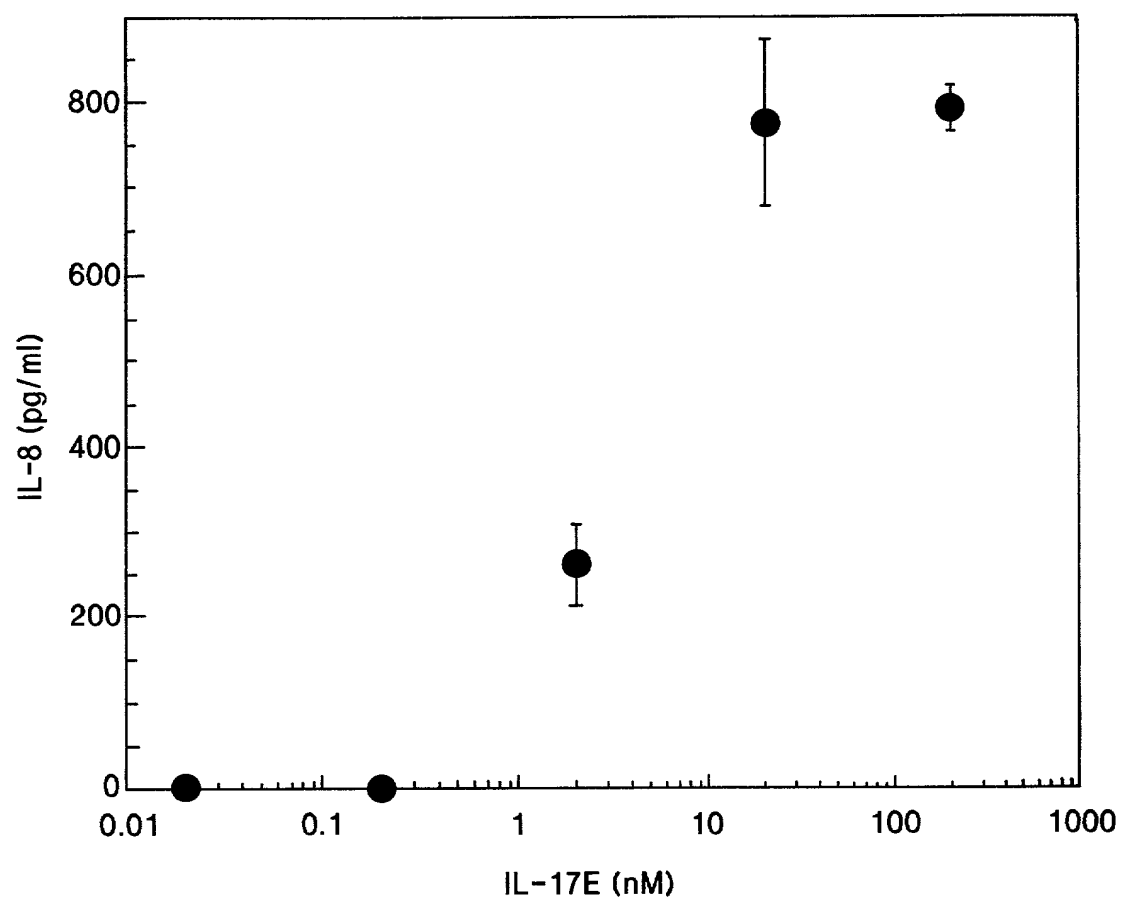


FIG. 34

IL-17 FAMILY OF CYTOKINES HAS COMPLEX PATTERN
OF OVERLAPPING RECEPTOR-LIGAND SPECIFICITIES

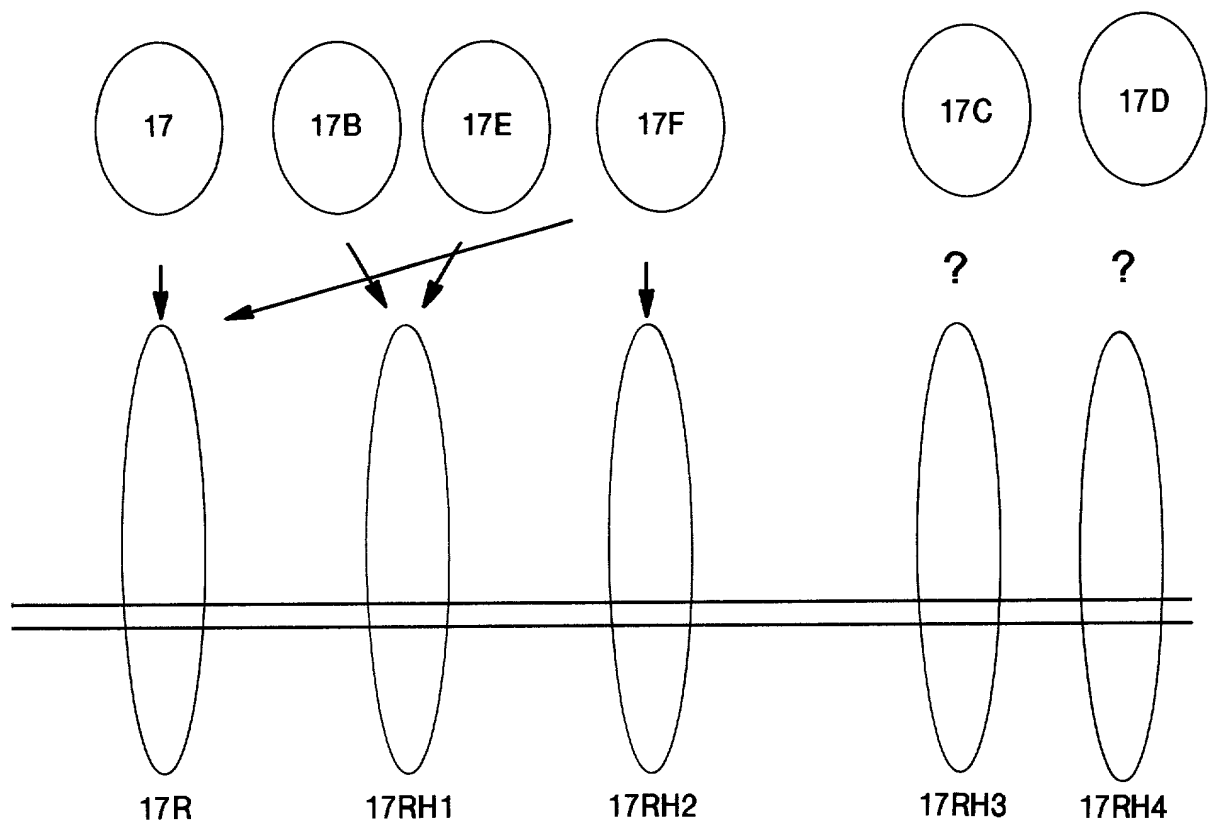


FIG. 35

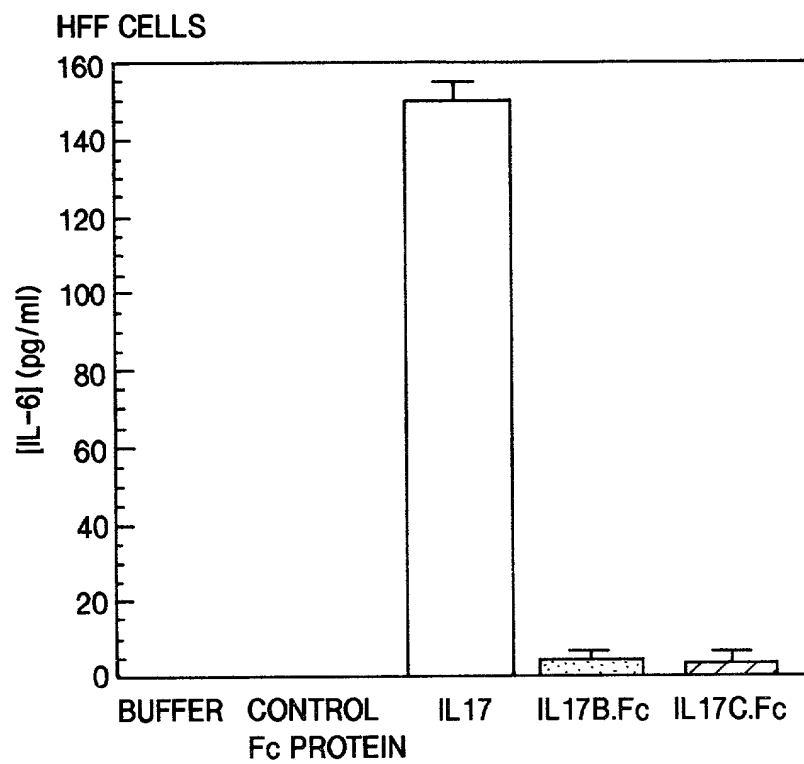


FIG. 36A

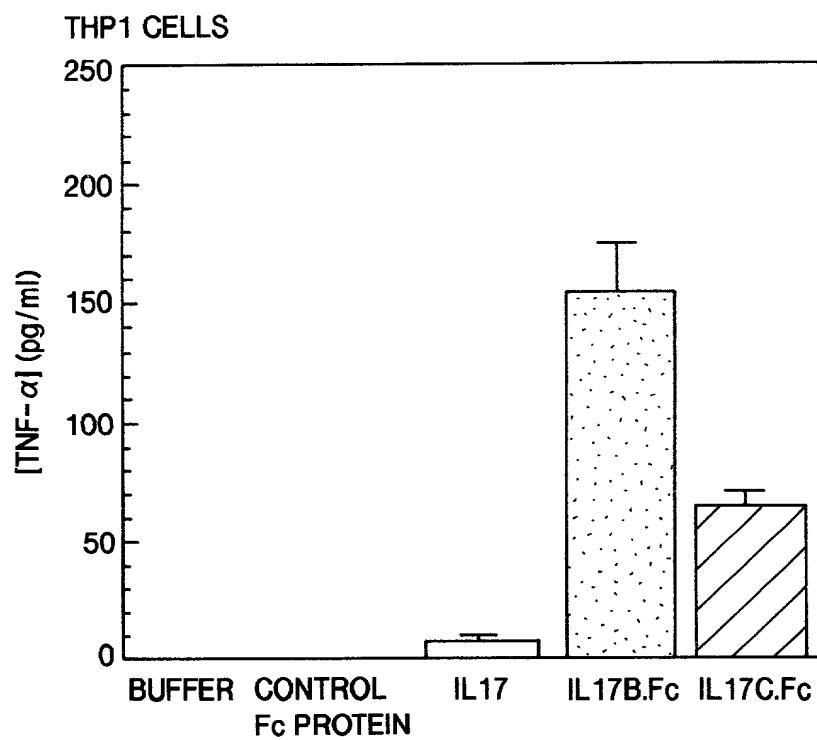


FIG. 36B

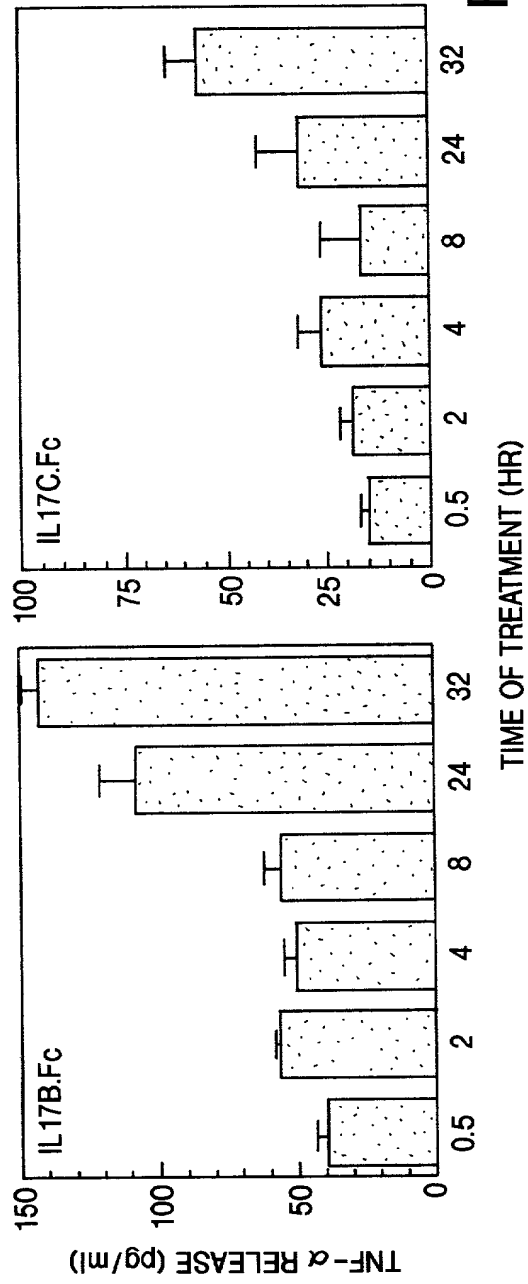


FIG. 37A

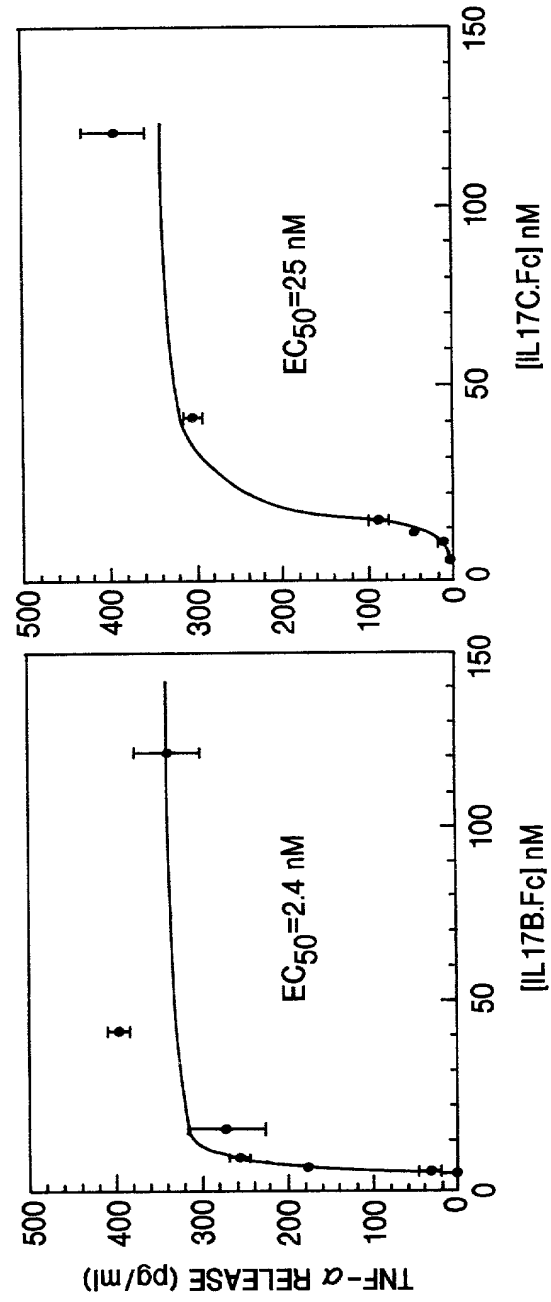


FIG. 37B

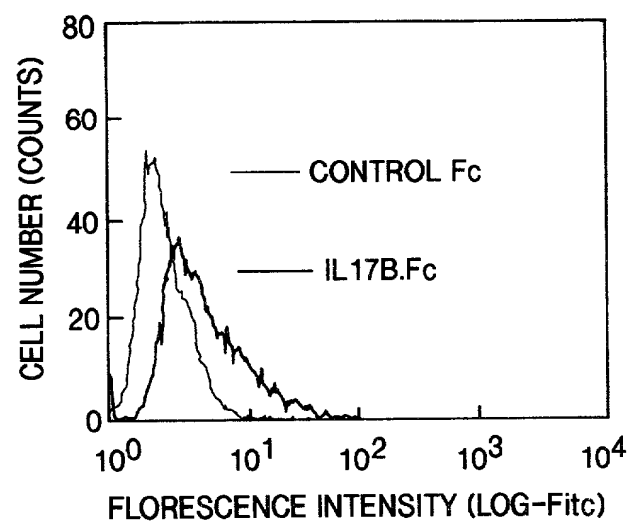


FIG. 38A

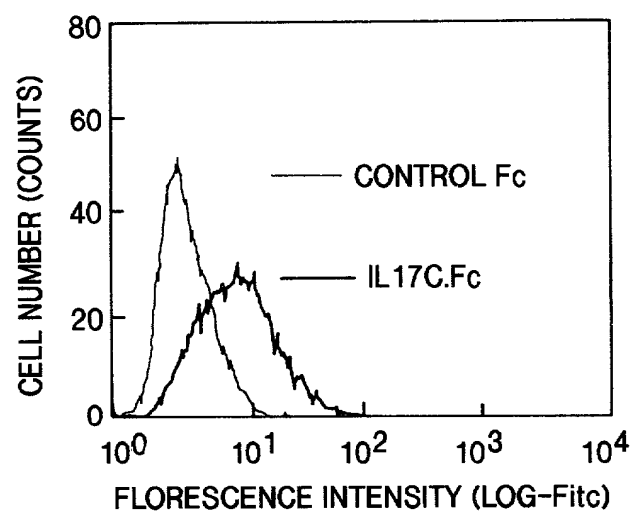


FIG. 38B

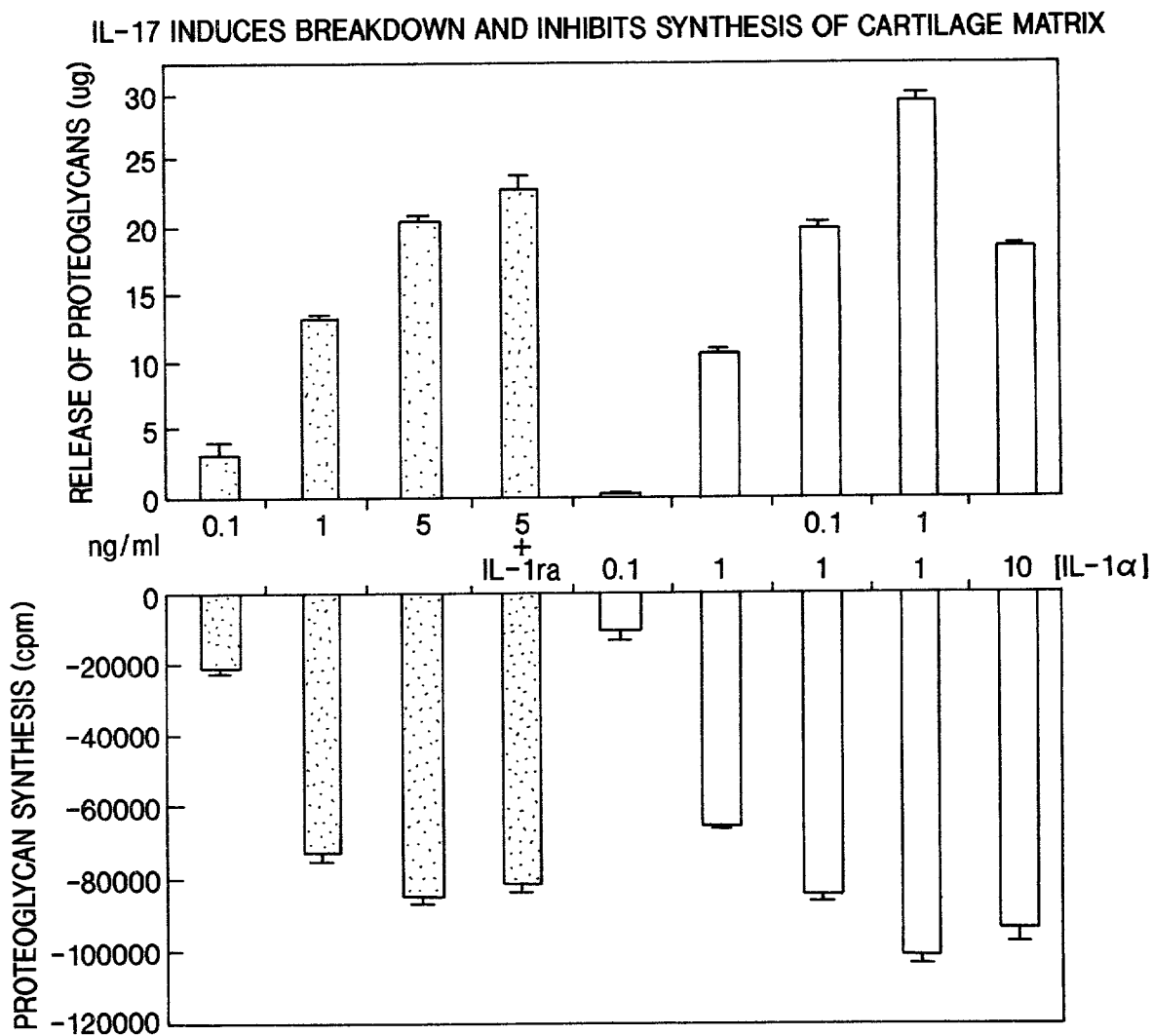


FIG. 39

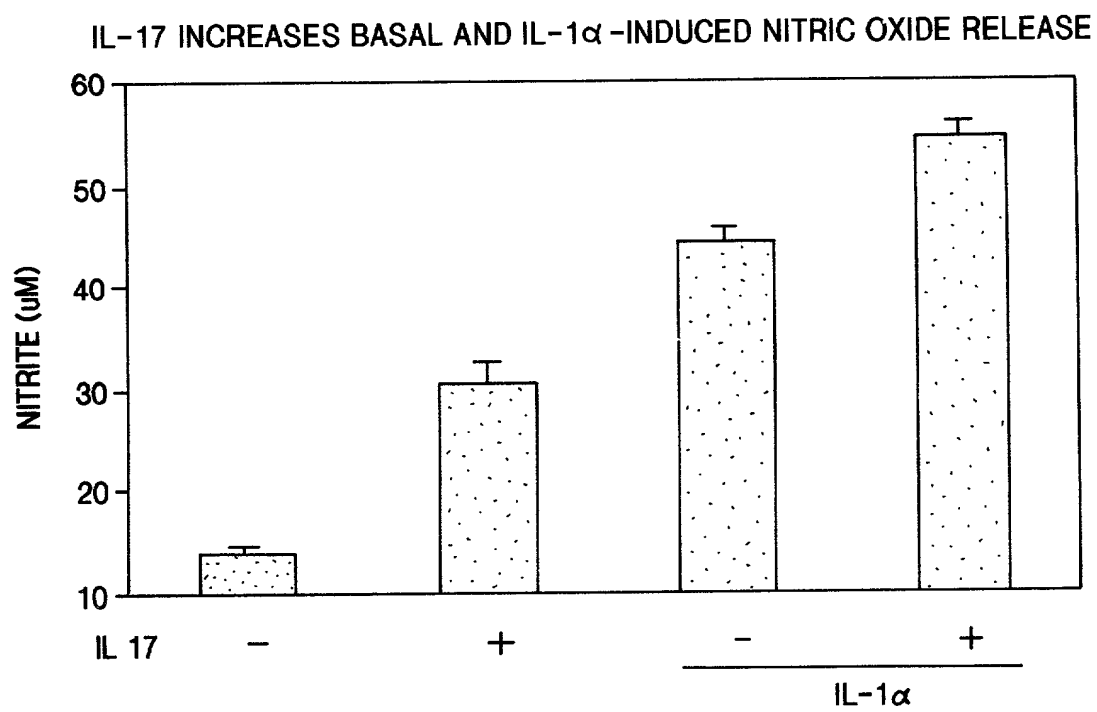


FIG. 40

INHIBITION OF NITRIC OXIDE RELEASE DOES NOT BLOCK THE DETRIMENTAL
EFFECTS OF IL 17 ON MATRIX BREAKDOWN OR SYNTHESIS

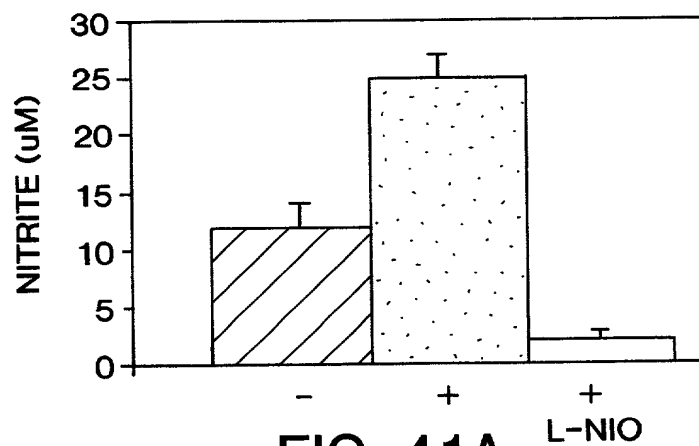


FIG. 41A

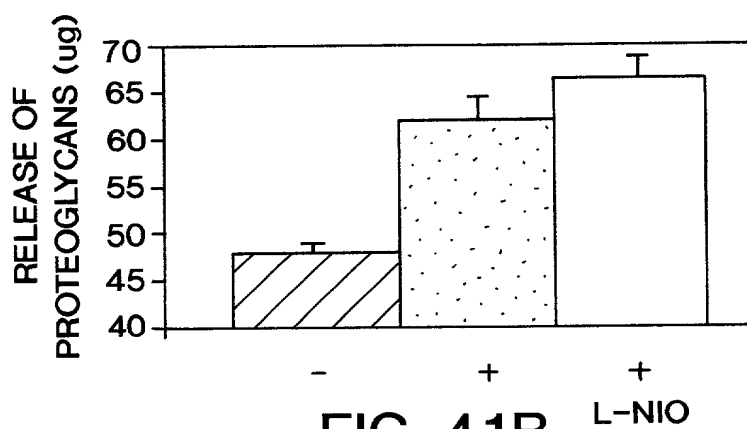


FIG. 41B

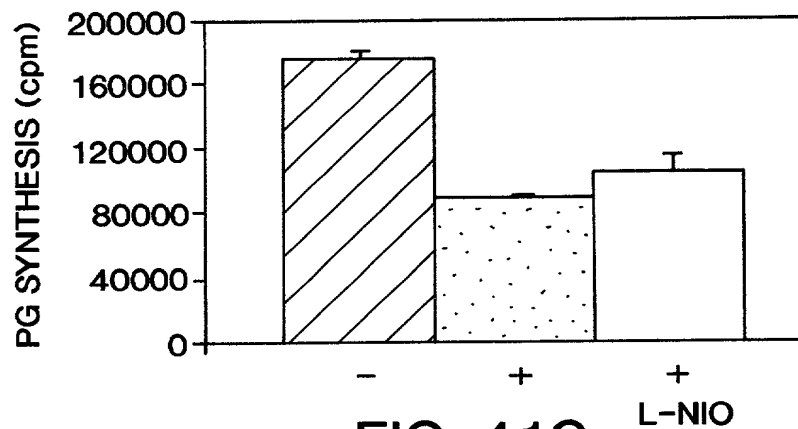


FIG. 41C

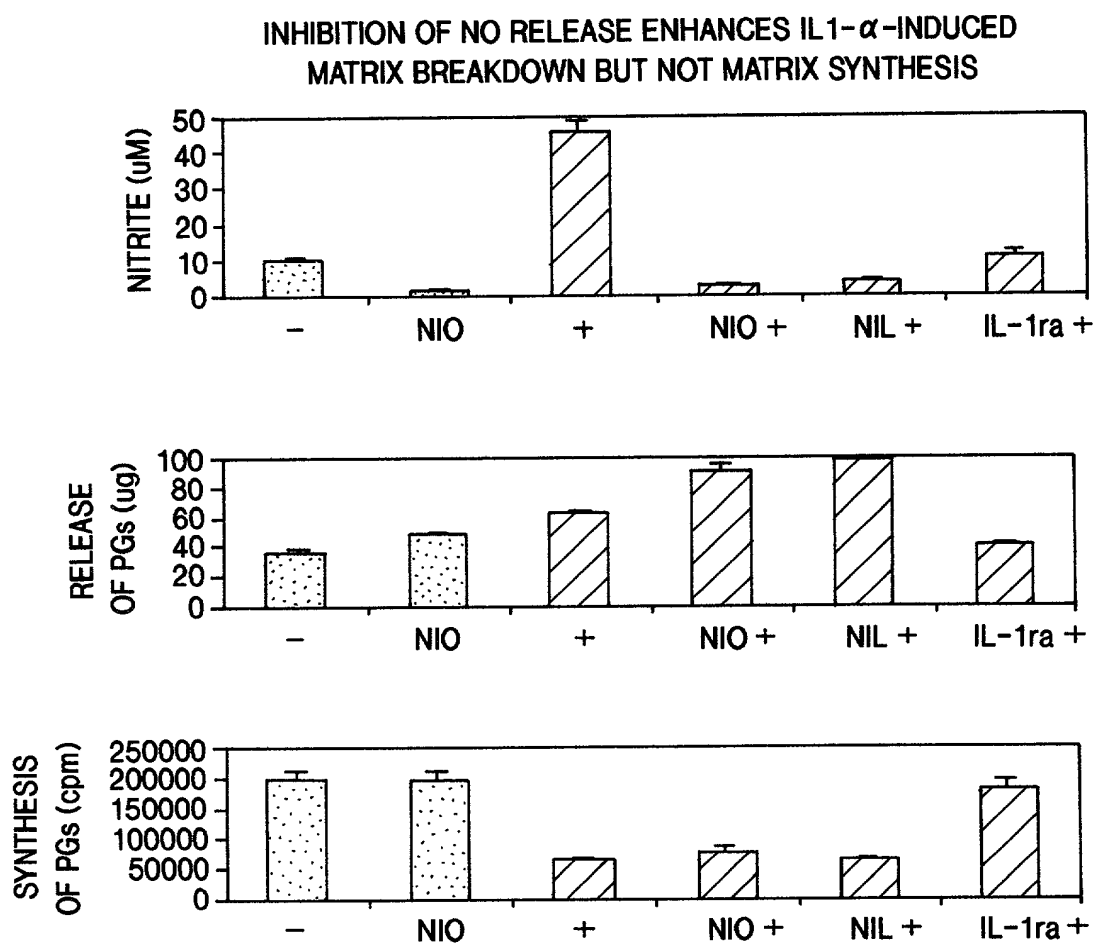


FIG. 42

IL-17C DETRIMENTAL EFFECTS ON ARTICULAR CARTILAGE

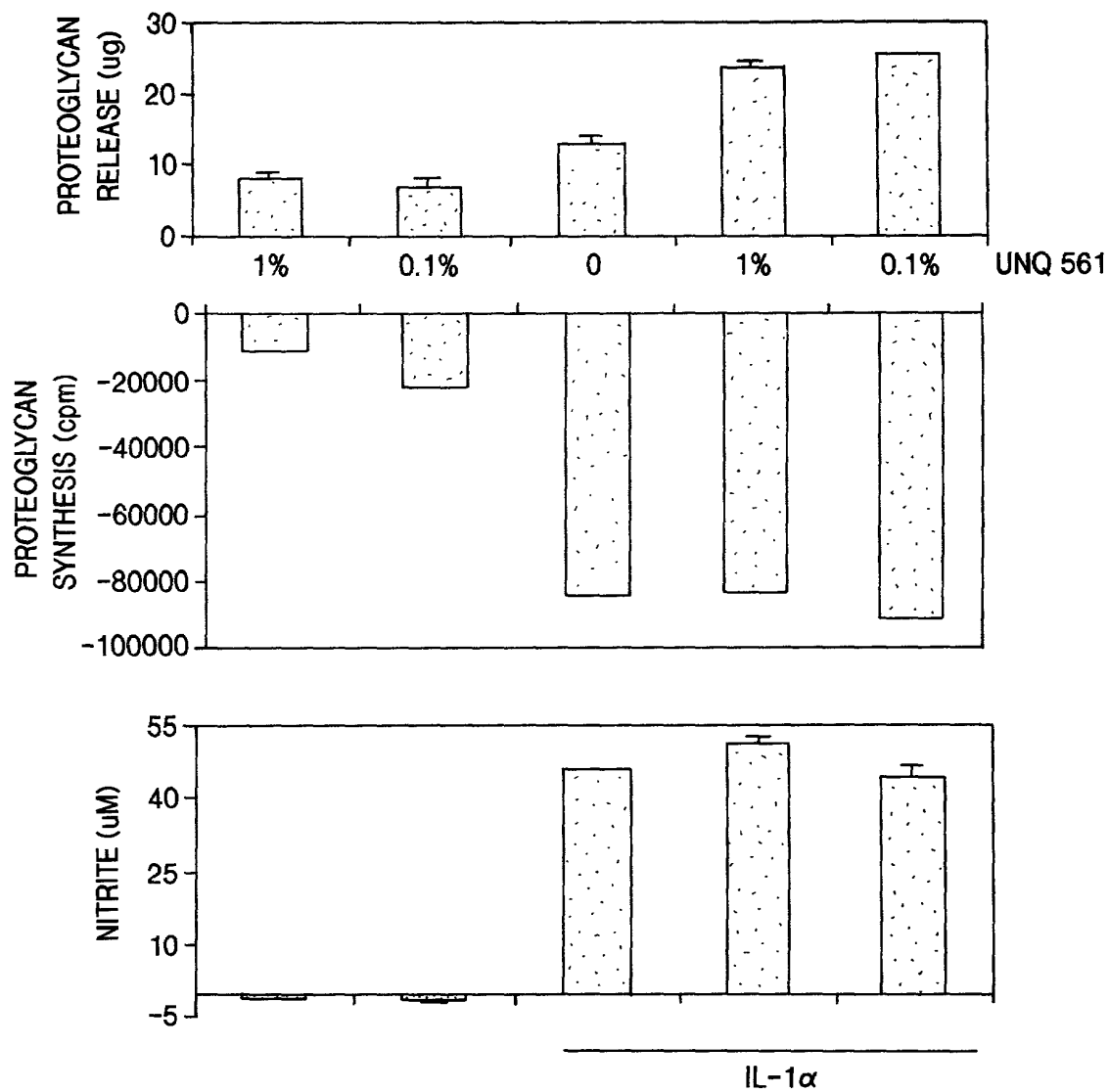


FIG. 43

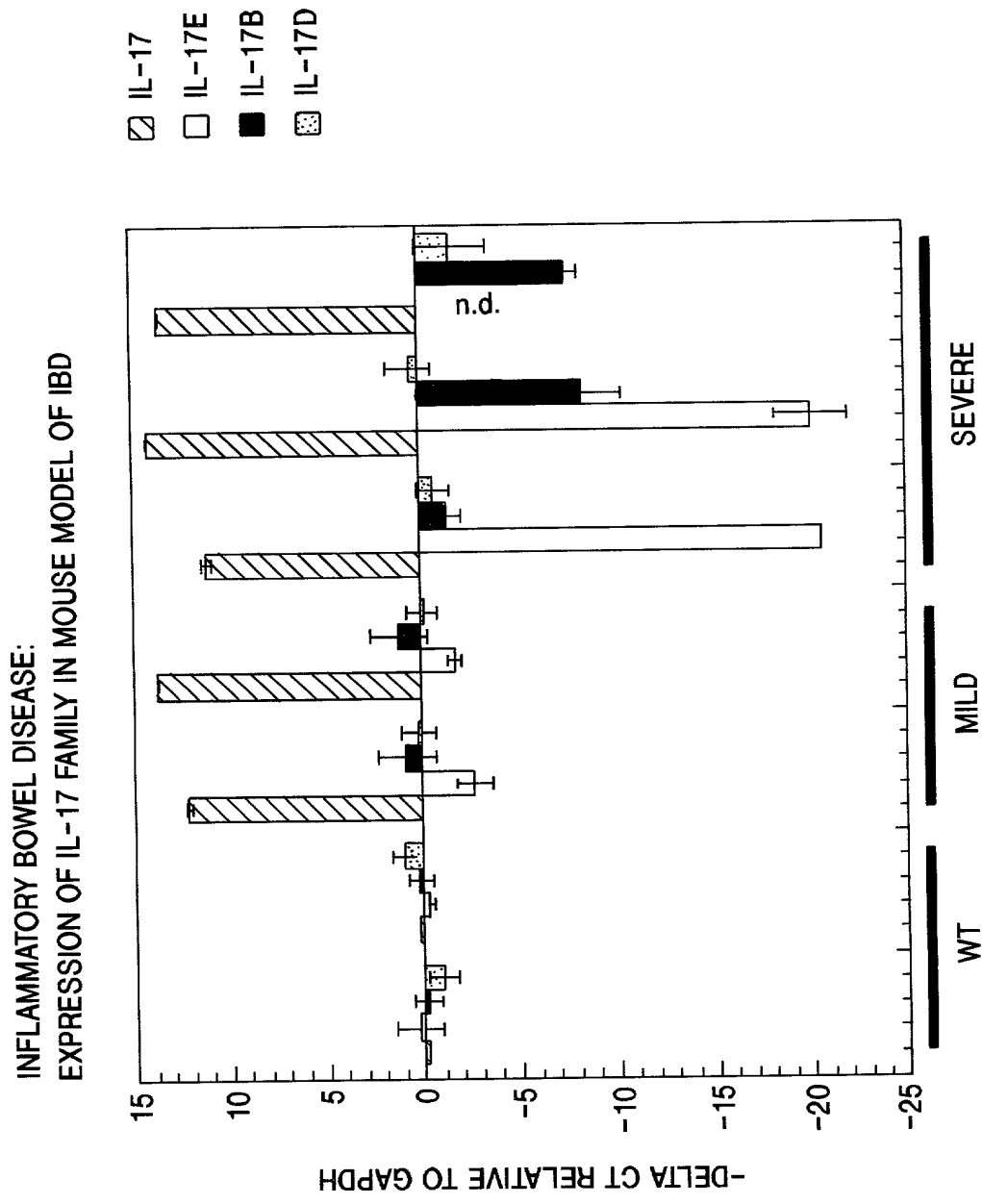


FIG. 44

IL-17D, PRESENT IN BRAIN, DECREASES RAPIDLY FOLLOWING STROKE

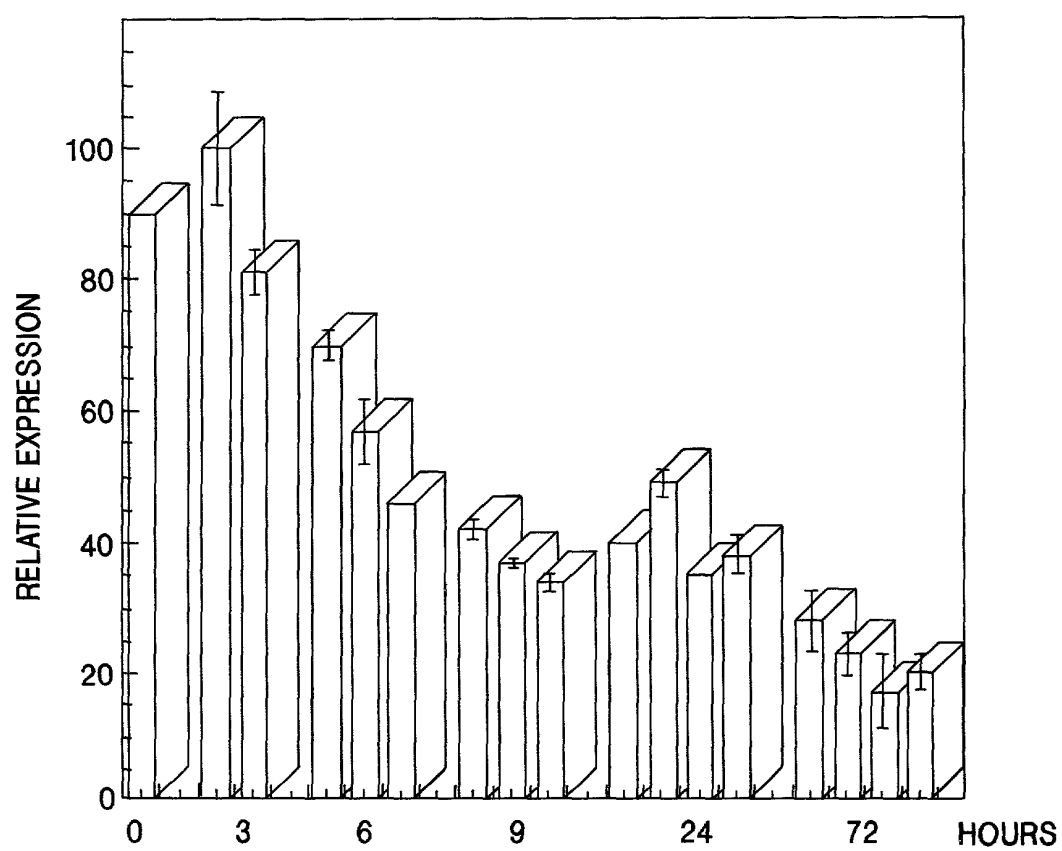


FIG. 45

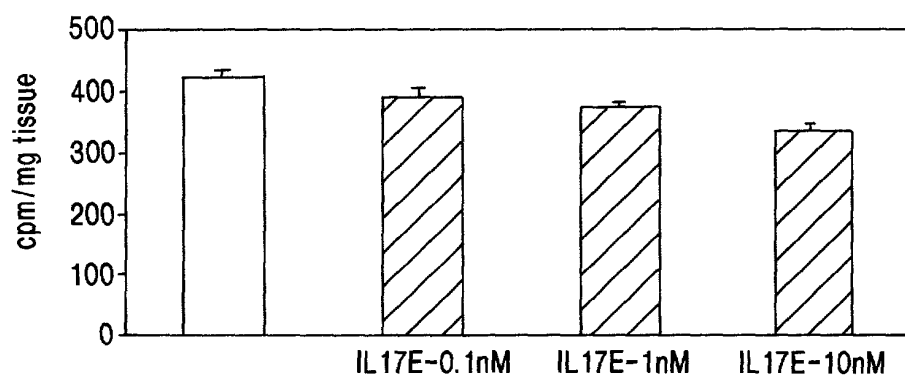


FIG. 46A

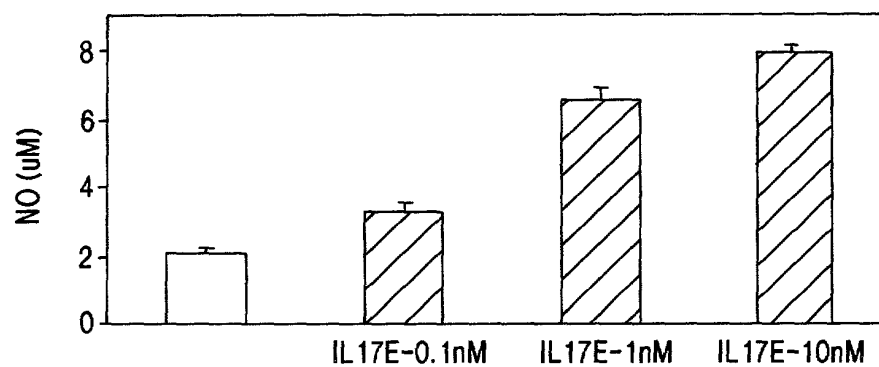


FIG. 46B

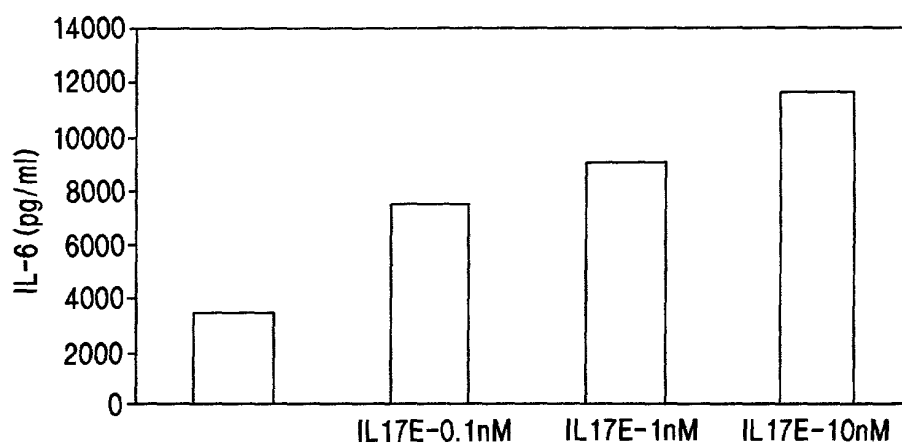


FIG. 46C

FIG. 47A

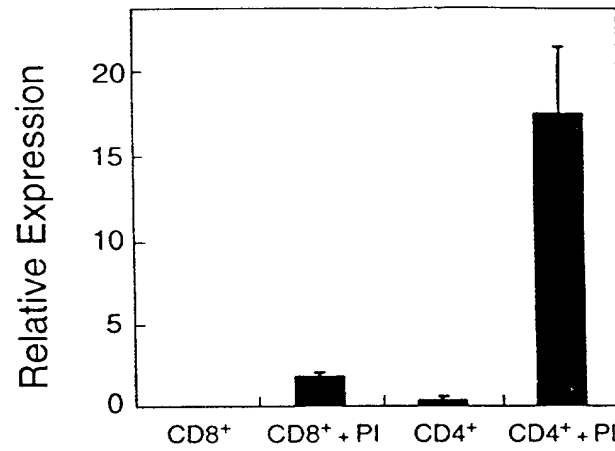


FIG. 47B

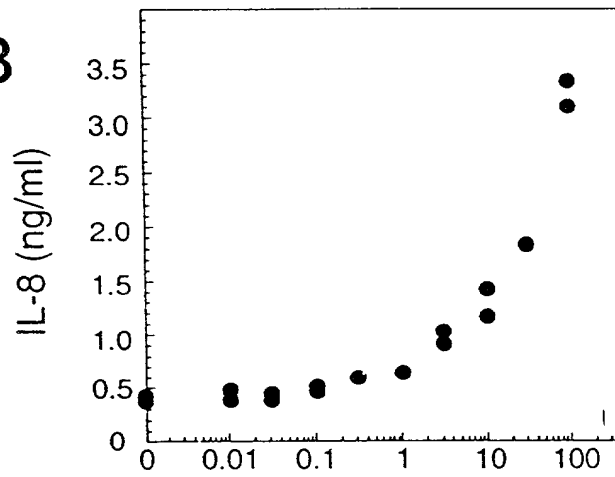
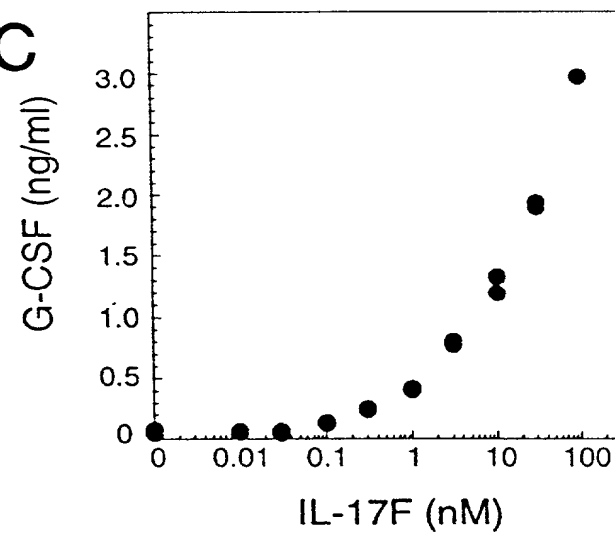


FIG. 47C



**Matrix
Breakdown**

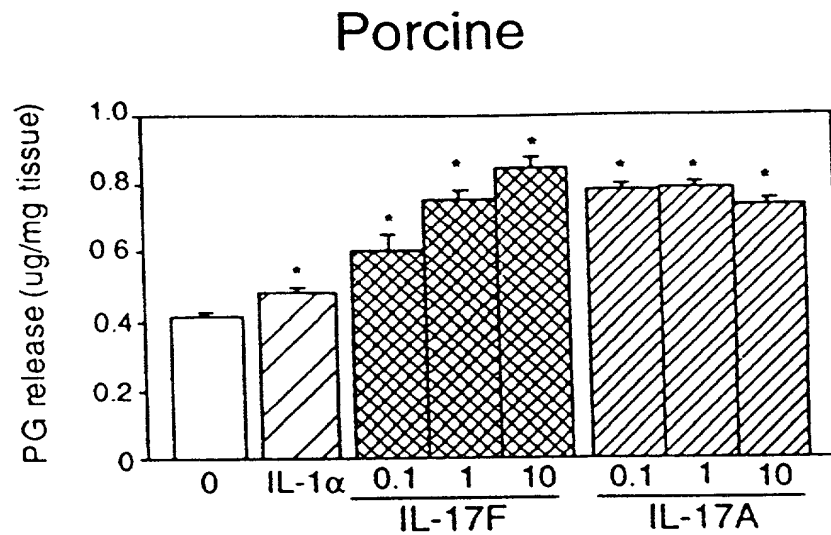


FIG. 48A

**Matrix
Synthesis**

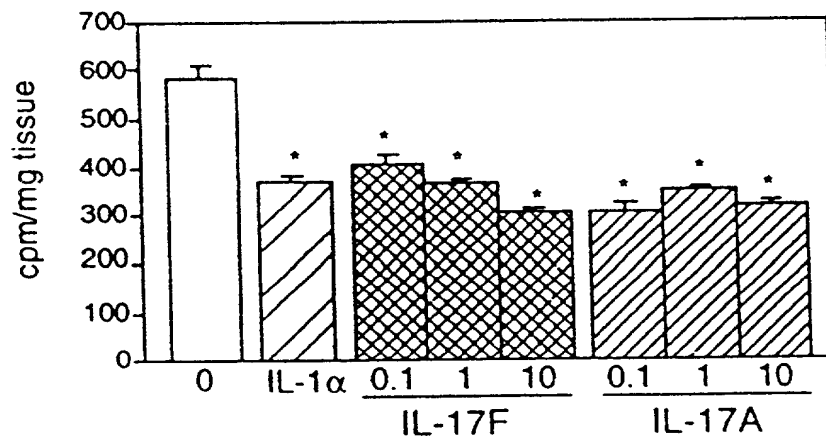


FIG. 48B

**IL-6
production**

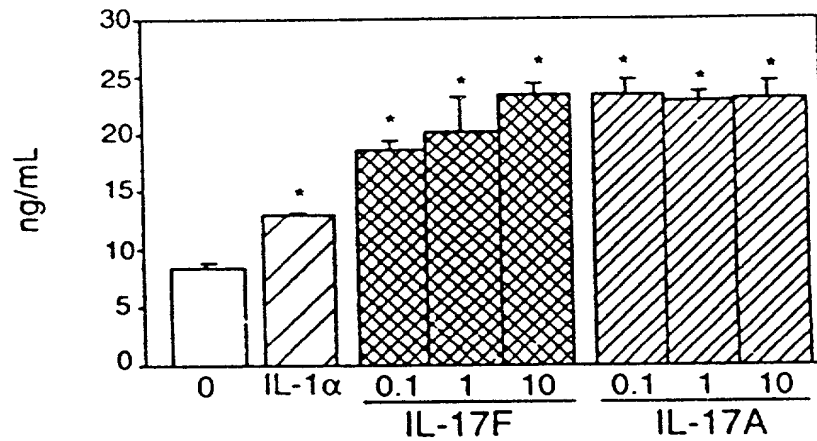


FIG. 48C

Human

Matrix Breakdown

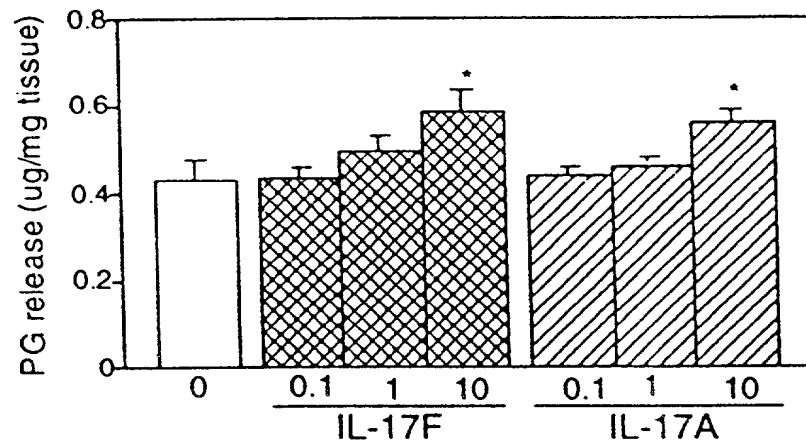


FIG. 48D

Matrix Synthesis

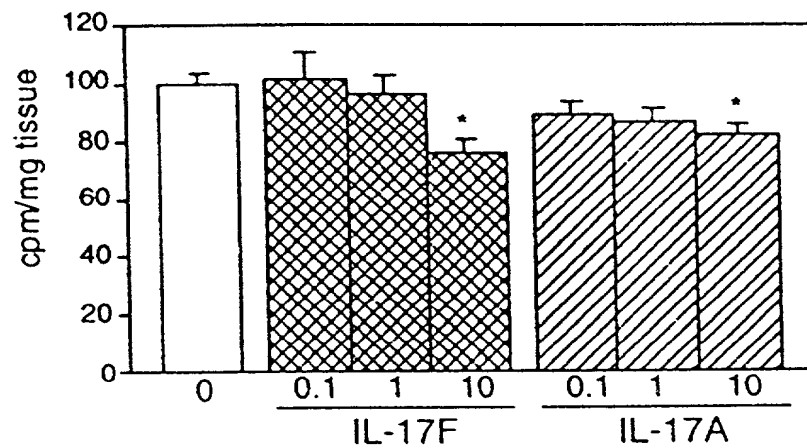


FIG. 48E

IL-6 production

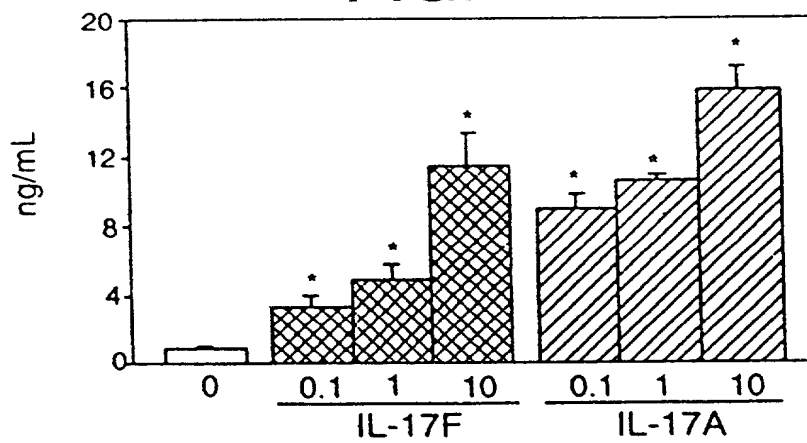


FIG. 48F

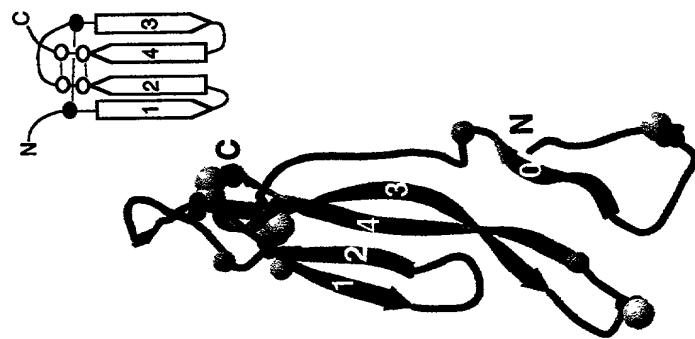


FIG. 49A

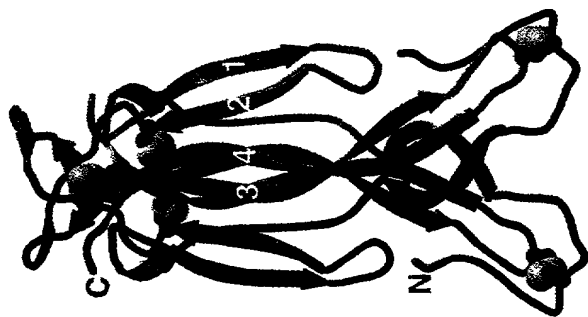


FIG. 49B

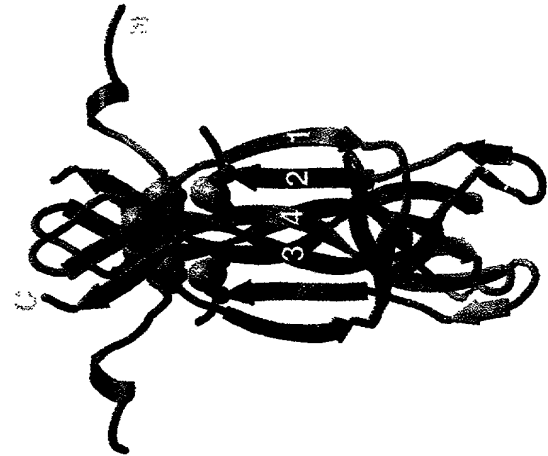


FIG. 49C

*

| | | | | | | |
|--------|-------------|-------------|------------|-------------|------------|----|
| IL-17F | | | |RKIPKVG | HTFFQKPES | 17 |
| IL-17A | | | |IVKAG | ITIPRNP.G | 14 |
| IL-17B |QPRS | PKSKRKQGR | PGPLAPGPHQ | VPLDLVSRMK | PYARMEEYER | 44 |
| IL-17C | HHDP SLRGHP | HS HGTPH YS | AEELPLGQAP | PHLLARGAKW | GQALPVALVS | 50 |
| IL-17E | | |YS | HWPS PSKG | QDTSEELLRW | 22 |

| | | | | | | |
|--------|------------|------------|-------------|------------|-----------|----|
| IL-17F | PPVPGG.... |SMKLDI | GIINENQVRS | MSRNIESRST | PWNYTWTWD | 59 |
| IL-17A | PNSEDKNFPR | TVMVNLNIHN | RNTNTN..PK | RSSDYNNRST | PWNLHNRD | 62 |
| IL-17B | NIEEMVAQLR | ..NSSELAQR | K EV....NL | QLWMSNKRSL | PWGYSINH | 88 |
| IL-17C | SLEAASHRGR | ..HERPSATT | Q PVL RPEEV | LEADTHQRSI | PWRYRVDTD | 98 |
| IL-17E | STVPVPPLP | ..ARPNRHPE | S RASE.... | .DGPLNSRAI | PWRYELDRD | 65 |

| | | | | | | |
|--------|------------|------------|------------|------------|-------------|-----|
| IL-17F | PNRYPSEVVQ | AQ RNLG IN | A..QKEDIS | MN VPI.QQE | TLVVRKHQ | 106 |
| IL-17A | PERYPVIWE | AK RHLG IN | A..DGNVDYH | MN VPI.QQE | ILVLRREPPH | 109 |
| IL-17B | PSRIPVDLPE | AR L LG VN | PF.TMQEDRS | MV VPV.FSQ | VPVRR...L | 133 |
| IL-17C | EDRYPQKLAF | AE L RG ID | AR.TGRETA | LN VRL.LQS | LLVLR...RP | 144 |
| IL-17E | LNRLPQDLYH | AR L PH VS | LQTGSHMDPR | GN ELLYHNQ | TVFYRRP...L | 112 |

*

| | | | | | | |
|--------|-----------|------------|-------------|-----------|-----|-----|
| IL-17F | SV..... |SFQLEK | VL..VTVG..T | VTPVIHVVQ | ... | 133 |
| IL-17A | PN..... |SFRLEK | IL..MSVG..T | VTPIVHVA | ... | 136 |
| IL-17B | PPPPRTGP. |RQRA | VMTI AVG..T | IF..... | ... | 160 |
| IL-17C | SRDGSGLPT | PGAFATHTF | TH..VPVG..T | V.LPRSVAA | ALE | 184 |
| IL-17E | HGEKGTHKG |Y LER | RLYRVSLA V | VRPRVMG.. | ... | 145 |

FIG. 50

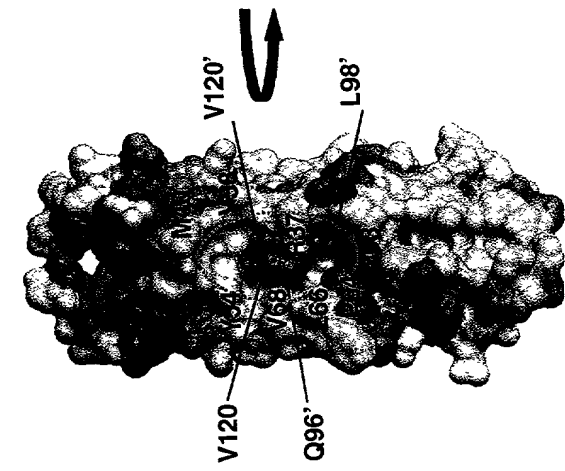


FIG. 51A

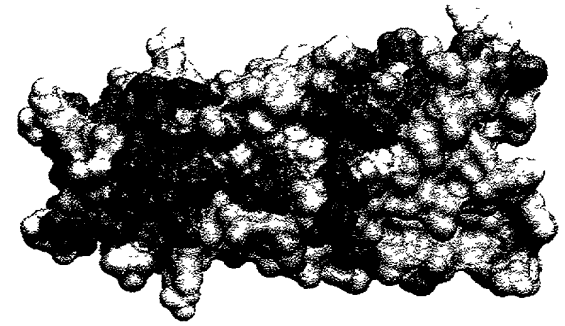


FIG. 51B

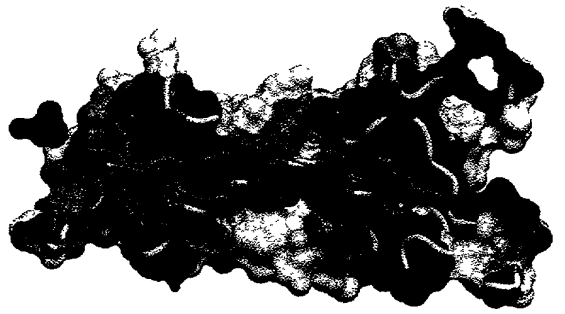


FIG. 51C

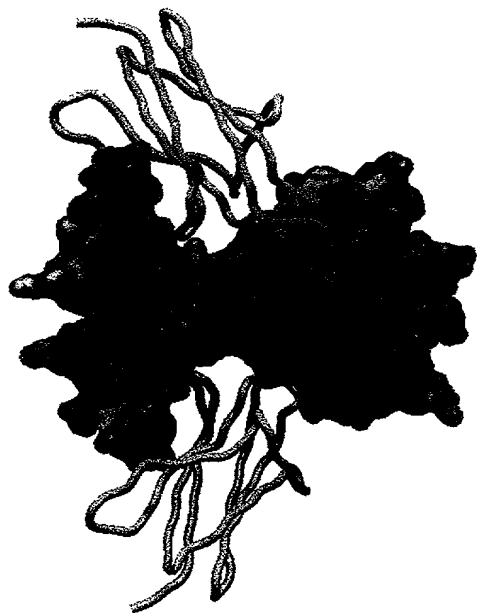


FIG. 52C

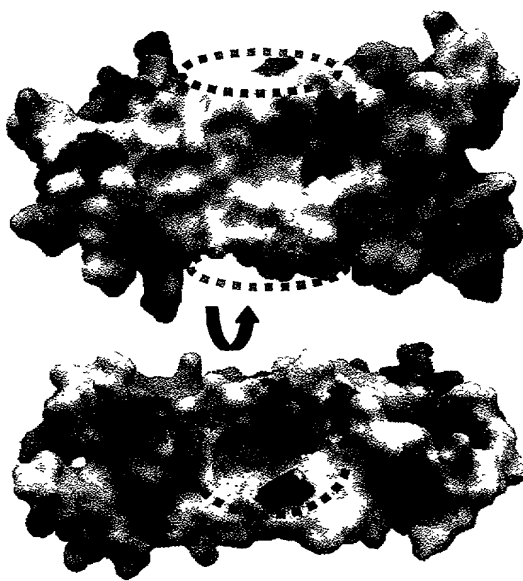


FIG. 52B

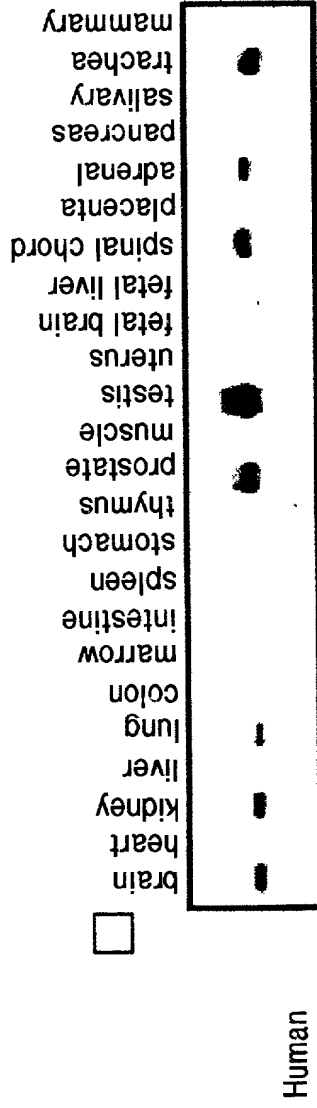
FIG. 52A

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---------|-----|-------|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| mIL-17E | 1 | ----- | VAF | L | A | M | I | V | G | T | H | T | V | S | L | R | I | Q | E | G | C | S | H | L | P | S | C | C | P | S | | | | | | |
| mIL-17E | 1 | MR | R | P | R | L | G | E | D | S | S | L | I | S | L | F | L | Q | V | V | A | F | L | A | M | V | M | G | T | H | T | | | | | |
| mIL-17E | 35 | K | E | Q | E | P | P | E | E | W | L | K | W | S | S | A | S | V | S | P | P | E | P | L | S | H | T | H | A | E | S | C | R | A | S | |
| mIL-17E | 43 | K | G | Q | D | T | S | E | E | L | L | R | W | S | T | V | P | V | P | P | L | E | P | A | R | P | N | R | H | P | E | S | C | R | A | S |
| mIL-17E | 85 | E | L | D | R | D | L | N | R | V | P | Q | D | L | Y | H | A | R | C | L | C | P | H | C | V | S | L | Q | T | G | S | H | M | D | P | |
| mIL-17E | 93 | E | L | D | R | D | L | N | R | L | P | Q | D | L | Y | H | A | R | C | L | C | P | H | C | V | S | L | Q | T | G | S | H | M | D | | |
| mIL-17E | 135 | R | P | C | H | G | E | E | G | T | H | R | R | Y | C | L | E | R | R | L | Y | R | V | S | L | A | C | V | C | V | R | P | R | V | | |
| mIL-17E | 143 | R | P | C | H | G | E | K | G | T | H | K | G | Y | C | L | E | R | R | L | Y | R | V | S | L | A | C | V | C | V | R | P | R | | | |

IL-17E is highly conserved between human and mouse

FIG. 53

Tissue distribution of IL-17E



IL-17E (PCR then probed with cDNA)

FIG. 54B

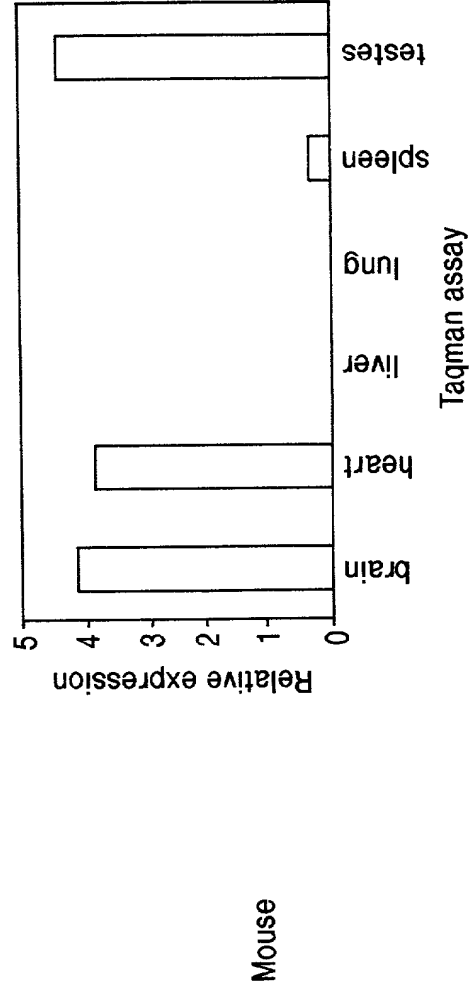


FIG. 54A

mIL-17E transgenics are growth retarded

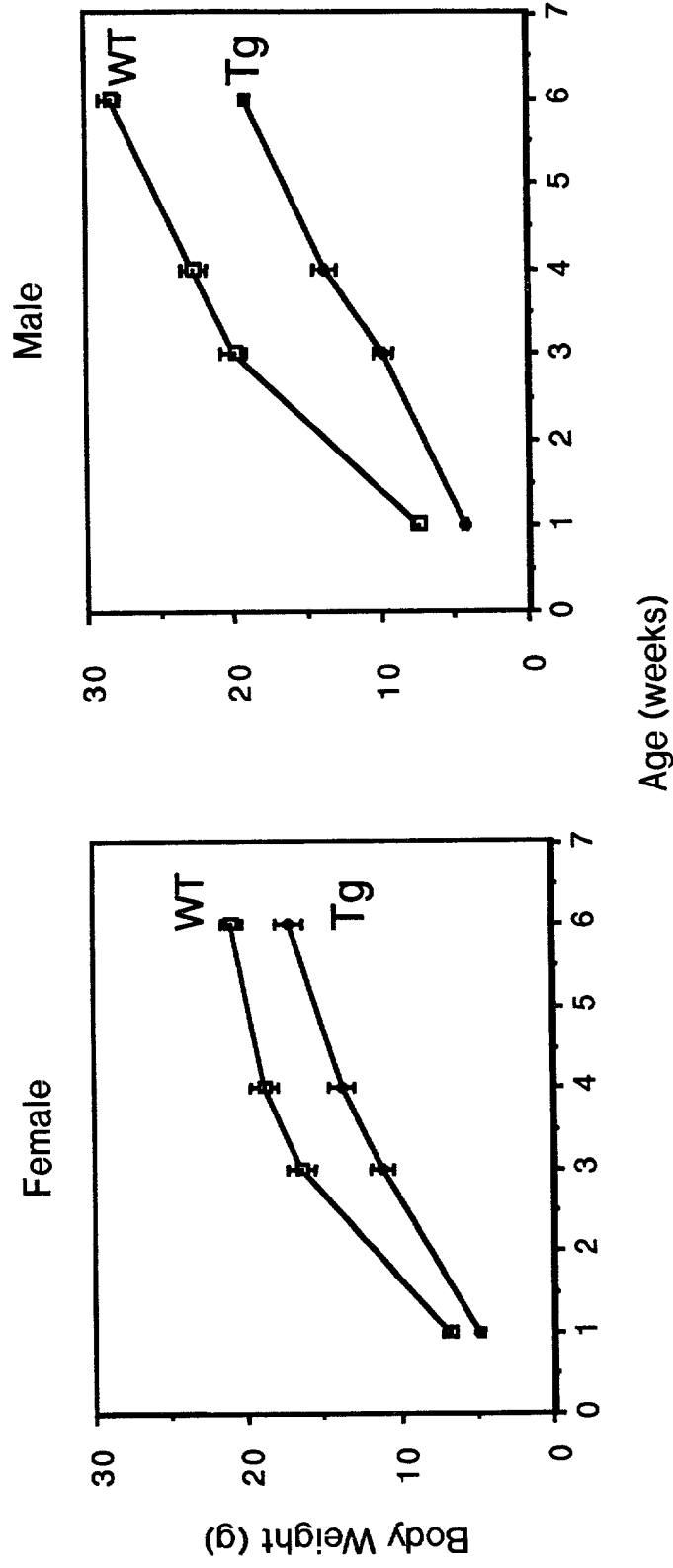


FIG. 55

IL-17E transgenics are jaundiced by 6 weeks of age



FIG. 56

mIL-17E transgenics have elevated total bilirubin and liver enzymes

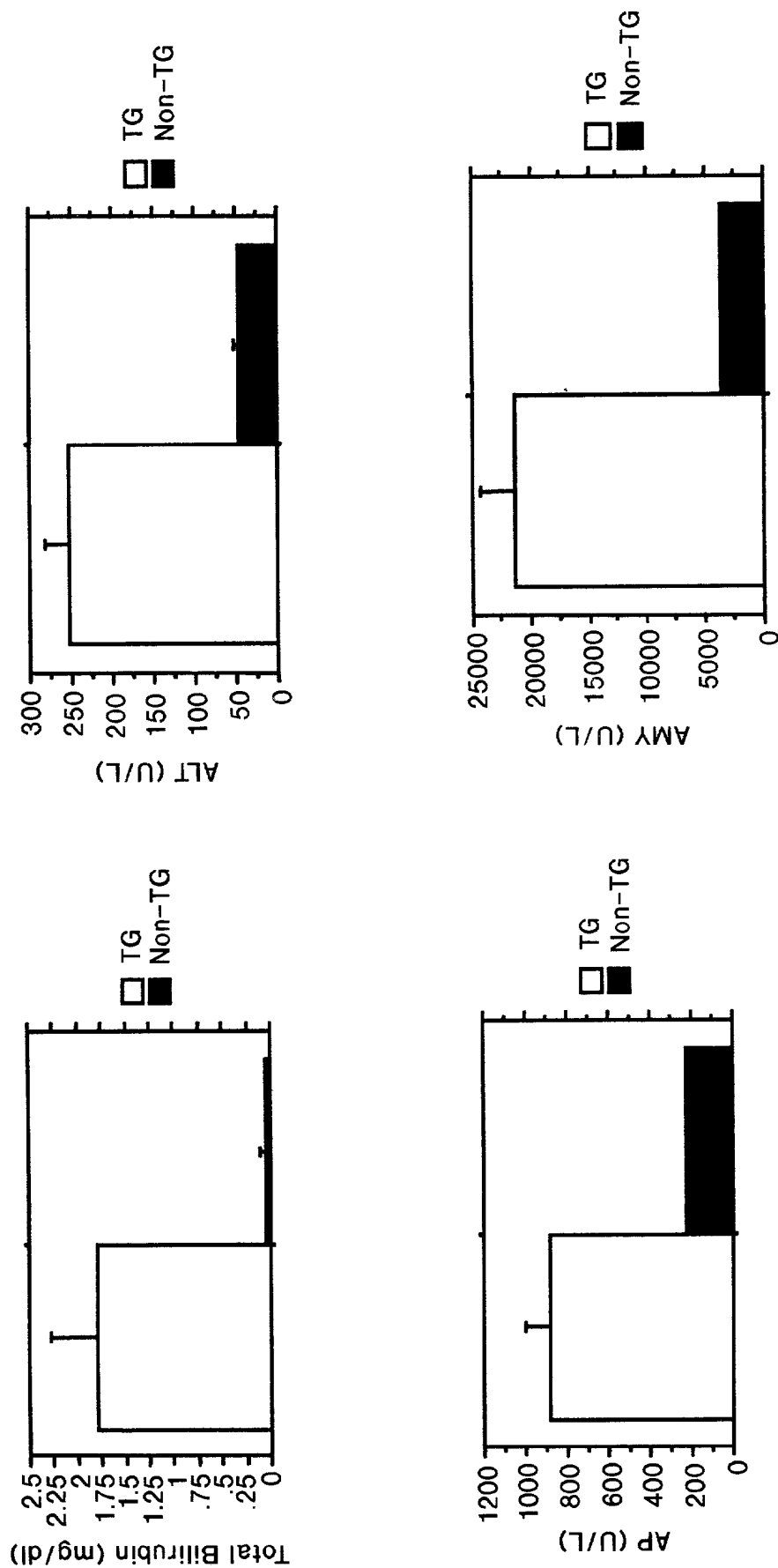


FIG. 57

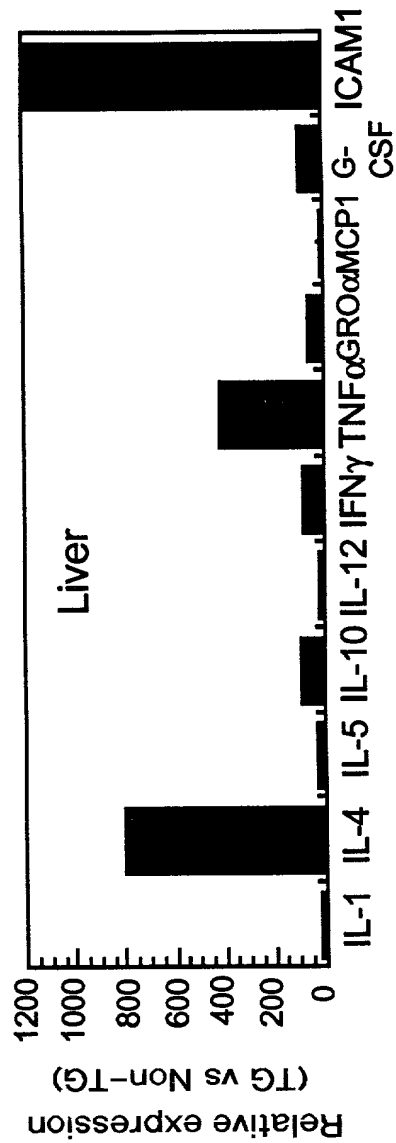


FIG. 58A

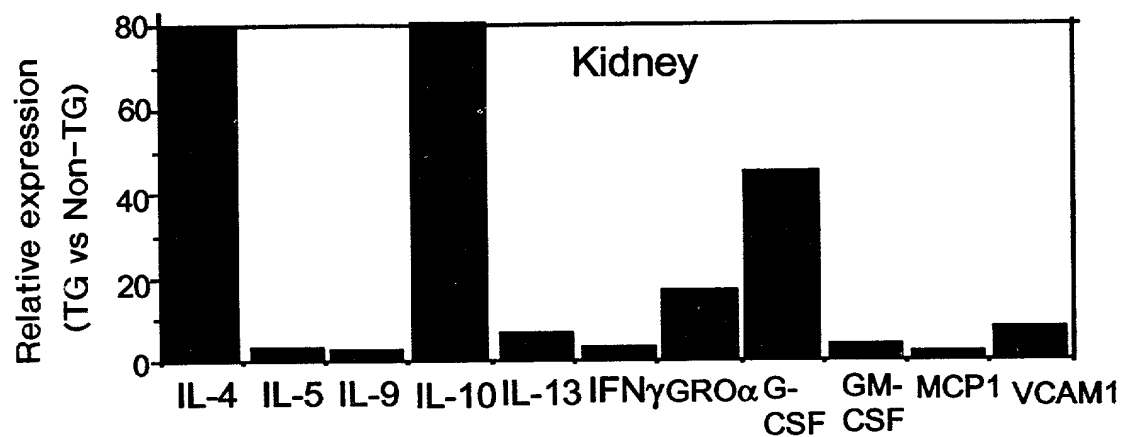


FIG. 58B

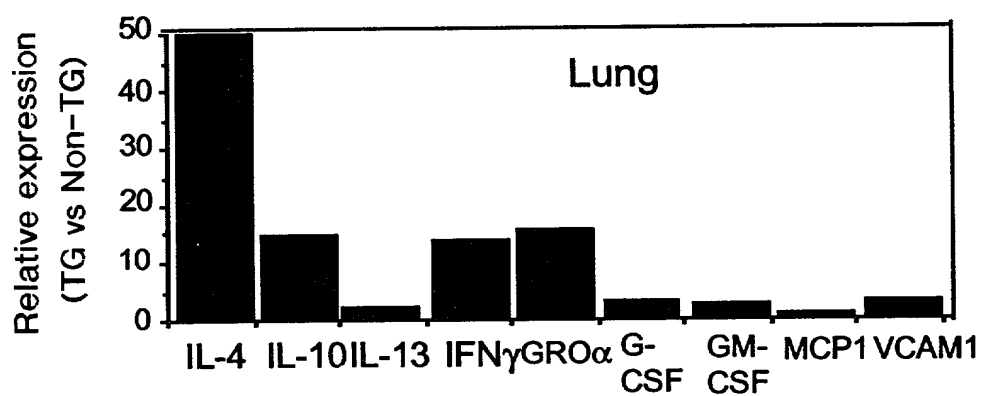


FIG. 58C

Gene profiling of IL-17E transgenics (Taqman)

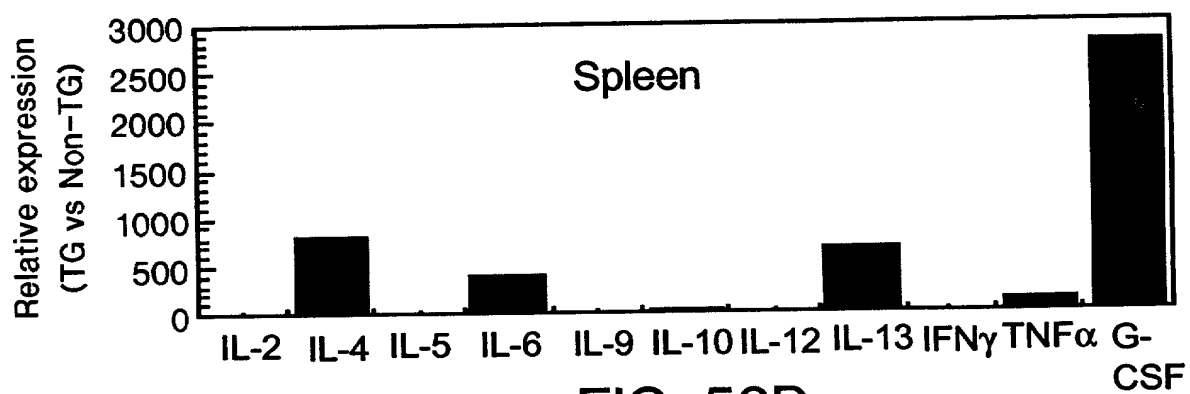


FIG. 58D

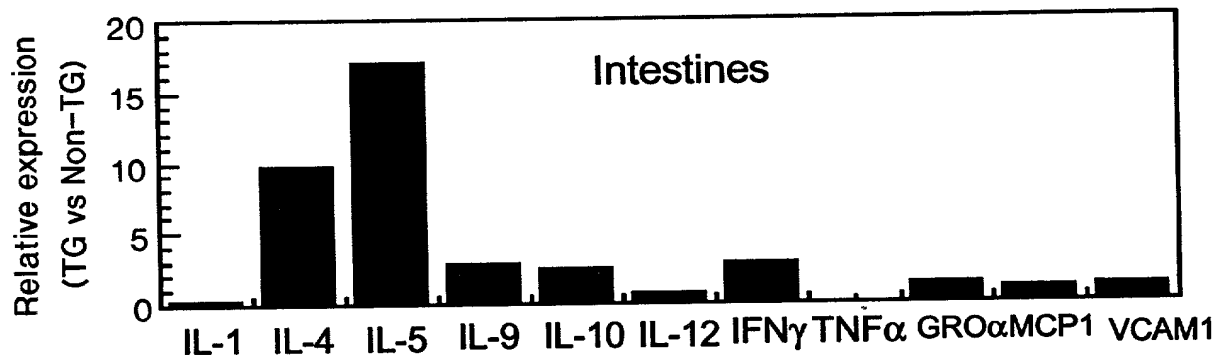


FIG. 58E

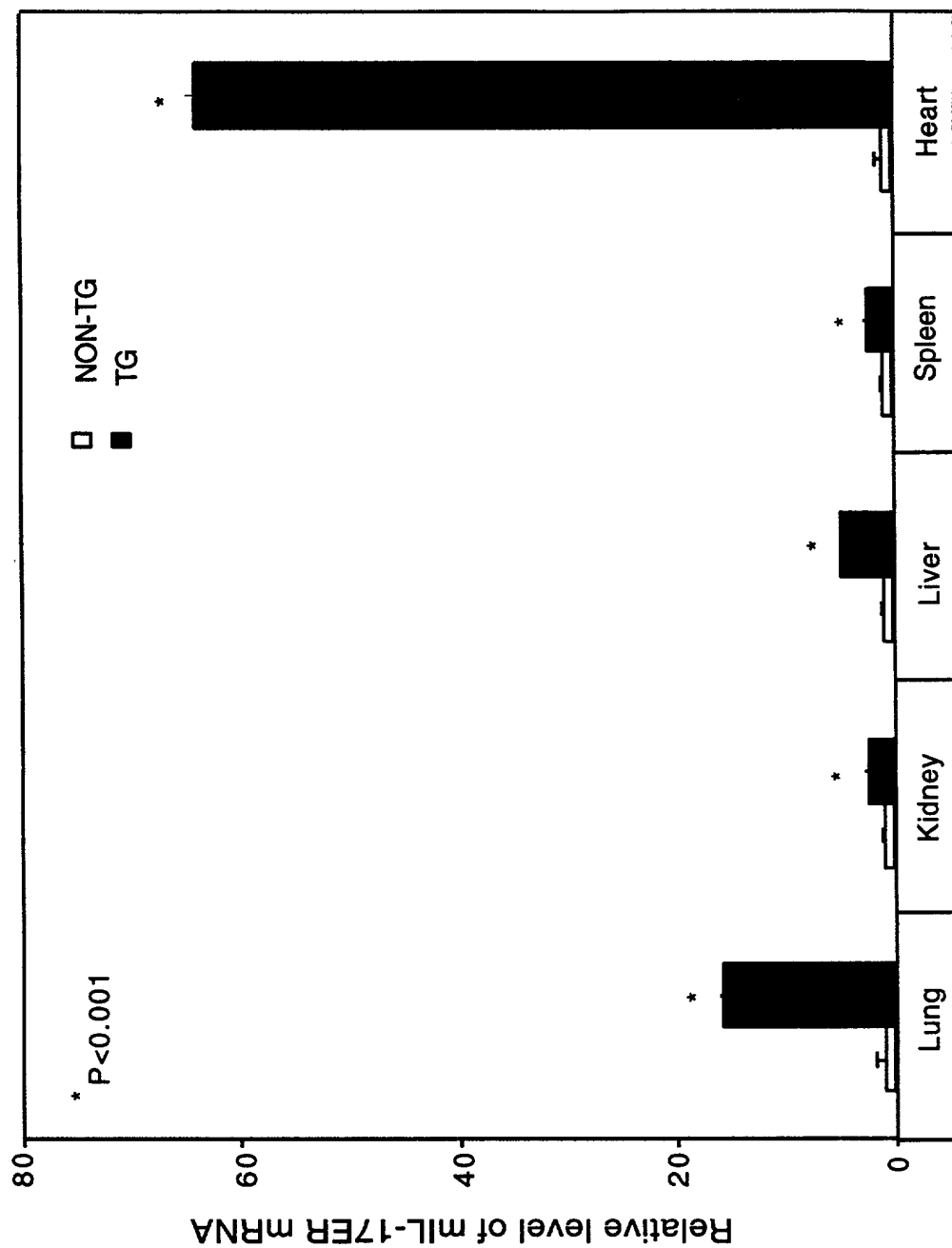


FIG. 59

Elevated serum IL-5, IL-13 and TNF α
in mIL-17E transgenics

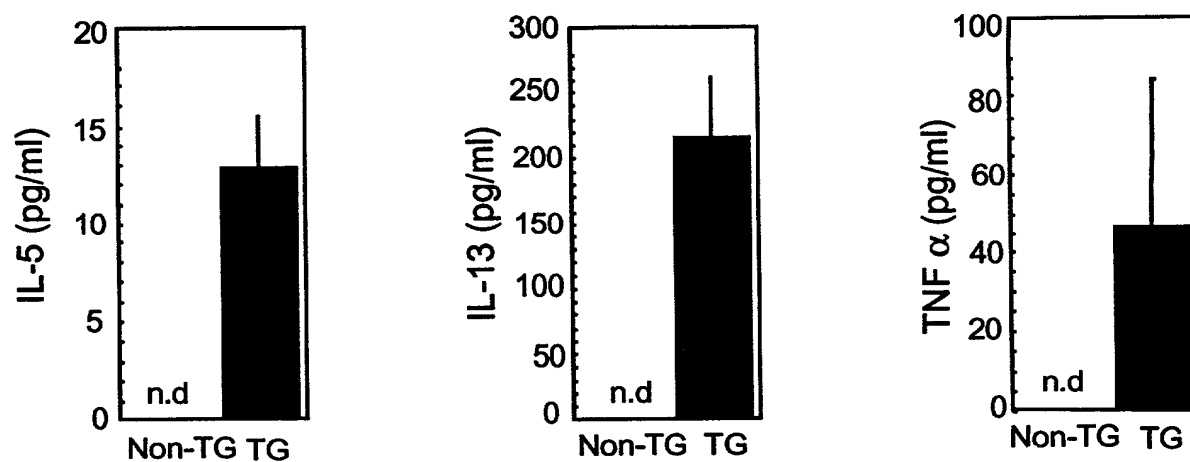


FIG. 60

Serum IgE and IgG1, but not IgG2a is elevated
in mIL-17E transgenics

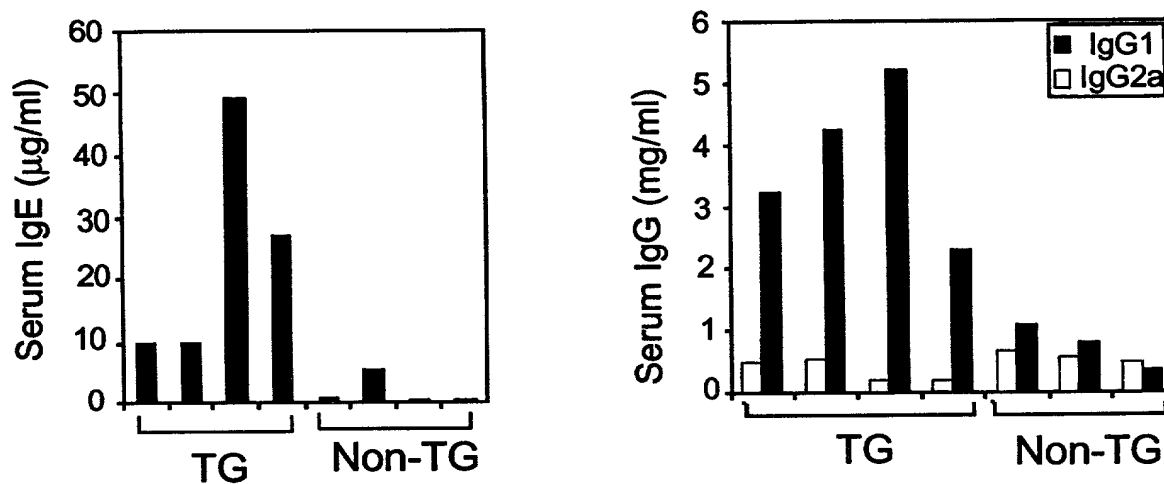


FIG. 61

Neutrophilia in mL-17E transgenics (8 wks, PBMC by FACS)

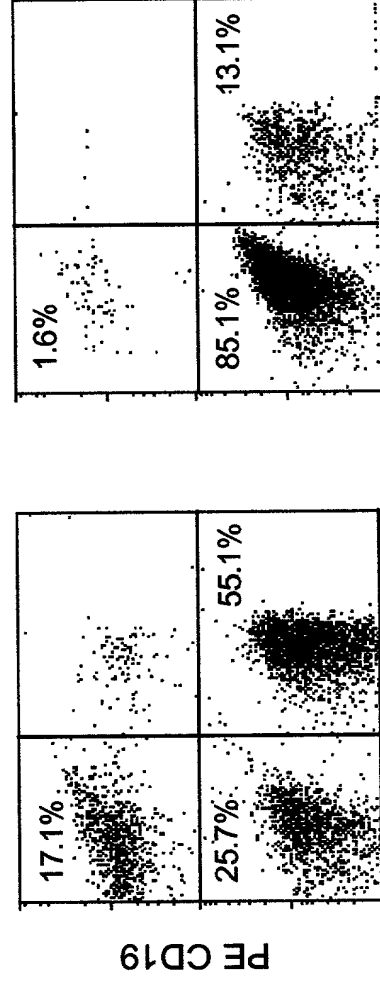


FIG. 62A

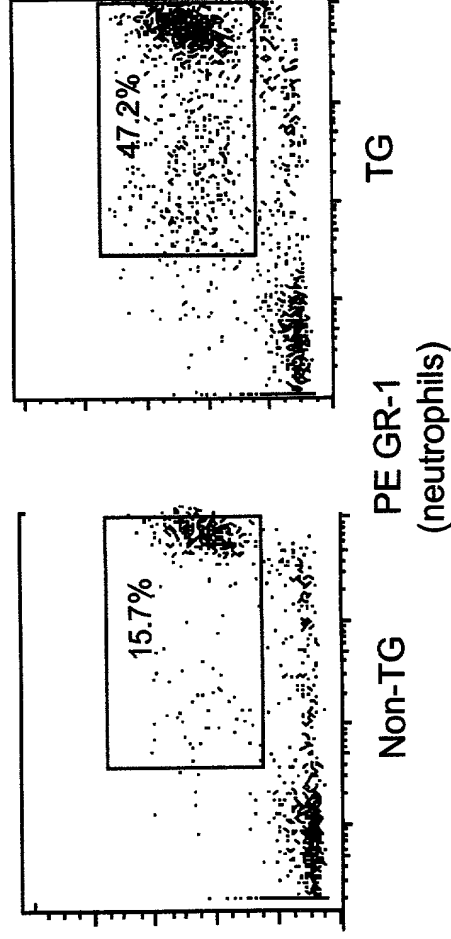


FIG. 62B

Neutrophilia and eosinophilia in mIL-17E transgenics (hematology)

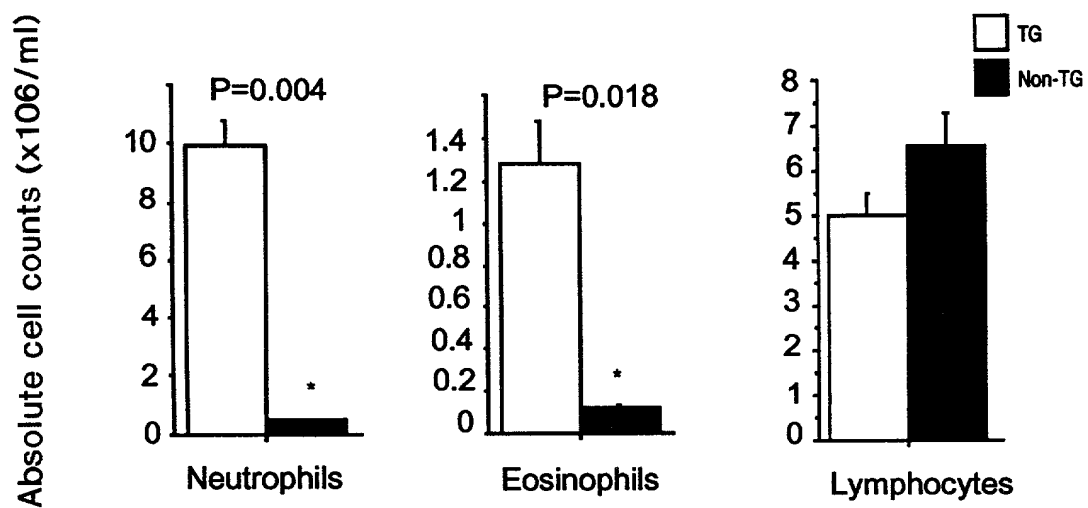


FIG. 63

G-CSF is elevated in
mIL-17E transgenics

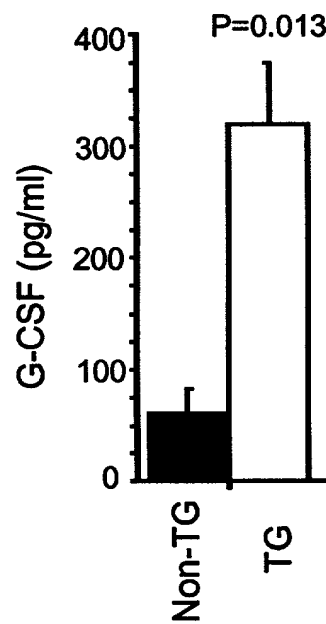


FIG. 64

IL-17E induces production of G-CSF in vitro

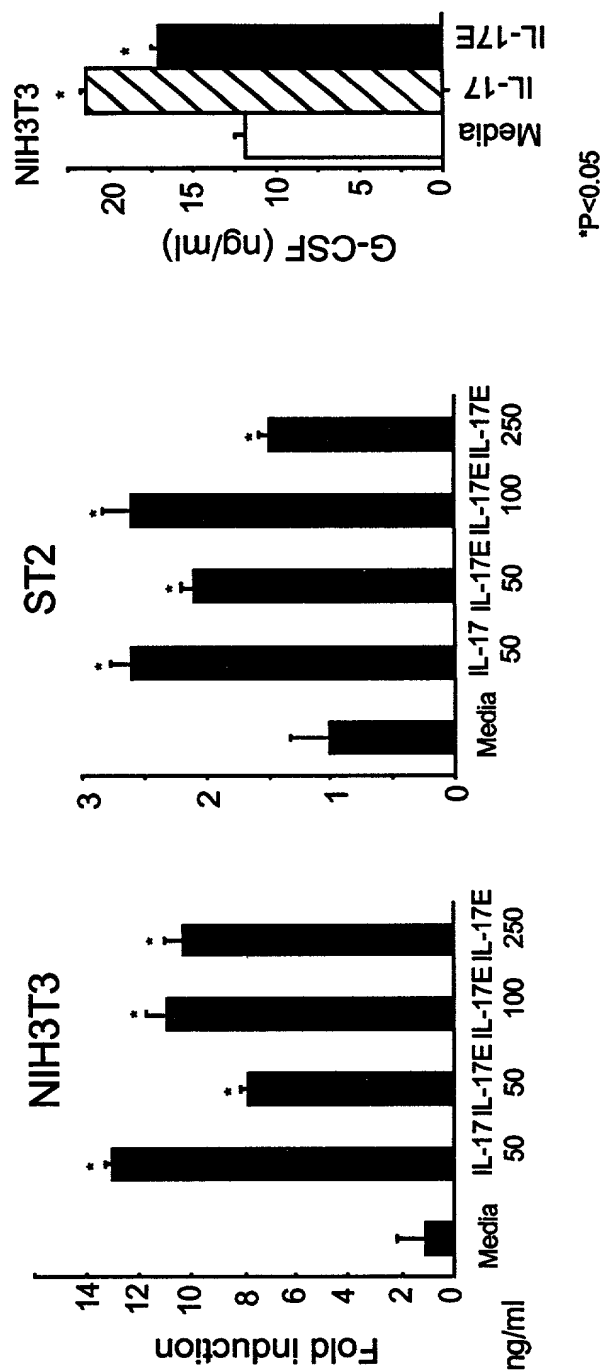


FIG. 65



FIG. 66A

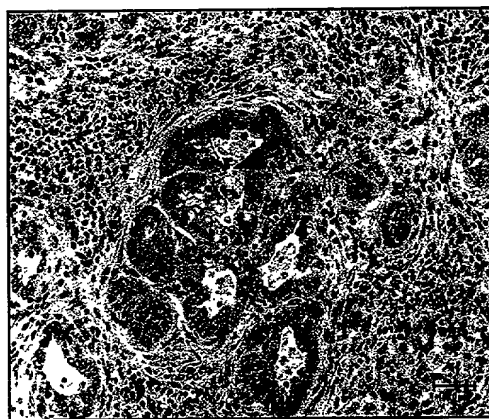


FIG. 66B

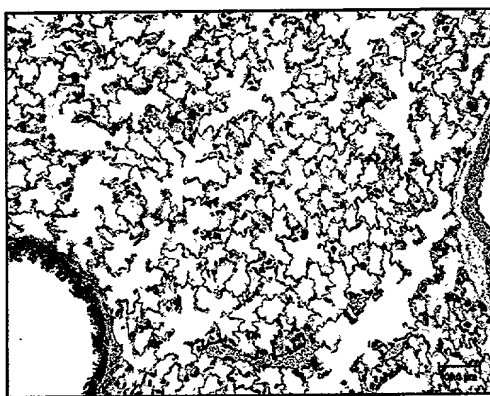


FIG. 66C

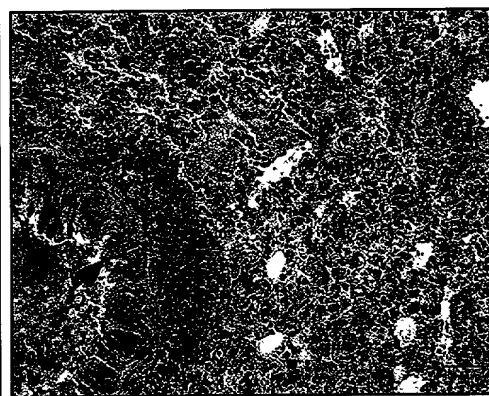


FIG. 66D